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January 13, 2006, 16:16:04; Search time 27.947 Seconds (without alignments) 1257.748 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2005s:\*

SUMMARIES

Ę,	Saposin-C	Human sap	Human Sap	Sphingoli	Human Pre	Human Sap	Нишап вар	Human sap	Human exp	Human DIT	Human GEN	Human cys	Amino aci	Human exp	Prosaposi	Human pro	Human pro	Lip-TAA b	Human exp	Human exp	Human exp	Human exp	Human exp	Human exp	
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ALIGNMENTS

RESULT 1  ARX70784  ID AAR70784 standard; protein; 80 AA.  XX  AC AAR70784;  XX  DT 25-WAR-2003 (revised)  DT 30-AUG-1995 (first entry)  XX  DE Saposin-C; neuron; myelination; nervous system; neuroblastoma; XX  XX  XX  Saposin-C; neuron; myelination; nervous system; neuroblastoma; XX  XX  Saposin-C; neuron; myelination; nervous system; neuroblastoma; XX  XX  Homo sapiens.  XX  PN W09503821-A1.  XX  PD 09-FEB-1995.  XX  PP 28-JUL-1994; 94WO-US008453.  XX  PR 30-JUL-1994; 94US-00100247.  PR 21-APR-1994; 94US-00232513.	IEN
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O'brien JS, Kishimoto Y;

WPI; 1995-082029/11. #X#X###X%XCCCCCCCCC

Stimulating neural cell out-growth and myelination - with pro:saposin, saposin C or new neurotrophic peptide(s) from cytokine(s), for treating nervous system diseases.

Disclosure, Page 32; 50pp; English.

The peptide given in AAR70773, corresponding to amino acids 8-29 of human saposin-C (AAR70784), promotes neurite outgrowth in vitro. A consensus sequence was determined by comparing the peptide with hematopoietic and neuropoietic cytokines, and neurotrophic peptides (AAR70774-82) were identified in the AB loop of human ciliary neurotrophic factor, interleukins-6, -2, -3 and -gamma, erythropoietin and leukocyte inhibitory factor, and in helix C of human interleukin-1-beta and oncostatin-M. Prosaponin (AAR7073) and saposin-C also promoted nerve cell myelination ex vivo. (Updated on 25-MAR-2003 to correct PN field.)

DRU- AVAILABEN CO

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61 ILLEEVSPELVCSMLHLCSG
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02-JUN-2000; 2000DK-00000865.
02-JUN-2000; 2000DK-00000866.
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1es 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prosaposin, saposin; prosaptides; prosaposin receptor agonists; PRA; peripheral nervous system; central nervous system; PMS; KTK; BC1-2; therapy; treatment; apoptosis; caspase; tumour necrosis factor; TNF; cytokine; interferon gamma; IRN; inflammation; rheumatoid arthritis; Crohn's disease; irritable bowel syndrome; asthma; cardiac infarction; acute disseminated inflammatory leukoencephalitis; progressive multifocal leukoencephalitis; progressive multifocal leukoencephalitis; Alzheimer's disease; garkingon's disease; duchance duchance duchance duchance duchance duchance duchance disease; duchance du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prosaposin is a 70kDa glycoprotein which is proteolytically processed to generate saposins A, B, C and D, all of which are similar to each other and have a similar placement of sar cysteines, a glycosylation site and conserved proline residues. Prosaposin, saposin C and prosaposin derived peptides (prosaptides), have therapeutic applications in promoting recovery after toxic, traumatic, mycardial ishchemic, degenerative and inherited lesions to the peripheral and central nervous system. Prosaposin receptor agonists (PRAs) inhibit prohifiammatory cytokine-induced apoptosis by activation of the Ser/Thr protein kinase Akt. Akt dissociates complexes of Ed. 2 family members, such as BAD-BG1-2, releasing BC1-2 and its family members which inhibit caspases, thereby
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(Updated on 25-WAR-2003 to correct PA field.) (Updated on 25-WAR-2003 to correct PI field.)
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                                                                                                                                               Length 80;
                                                                                                                                                                                              Indels
                                                                                                                                            100.0%; Score 412; DB 2;
100.0%; Pred. No. 2.4e-40;
ive 0; Mismatches 0;
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                                                                                                                                               Query Match
Best Local Similarity
Matches 80; Conserv
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                                                                                                Sequence 80 AA;
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cc inhibiting apoptosis. An additional mechanism whereby PRAs inhibit apoptosis is by blocking activation of JNK, a proapoptotic signaling component. Within several minutes after binding to the receptor, PRAs component. Within several minutes after binding to the receptor, PRAs block INK activation induced by tumor necrosis factor-alpha (INF alpha: Induced, as well as other proinflammatory cytokine-induced cappasse-mediated or induced by a proinflammatory cytokine-induced apoptosis. The method can be used for inhibiting apoptosis which is caspasse-mediated or induced by a proinflammatory cytokine, for example CT TNF alpha or interferon-gamma. It can be used for inhibiting apoptosis associated with a disorder such as e.g. rheumatoid arthitis, Crohn's cdisease, irritable bowel syndrome, asthma, cardiac infarction, congestive cdisease, irritable bowel syndrome, asthma, cardiac infarction, congestive collectes parkinson's disease, authoritoral leukoencephalitis, Alzheimer's disease, ischemic heart disease, Guillain-Barre disease, traumatic prain cord injury, traumatic spinal cord injury, alopecia, AlbS dementia, cerebral cord injury, traumatic spinal cord injury, alopecia, AlbS dementia, cerebral cord injury, traumatic spinal cord injury, alopecia, AlbS dementia, cerebral cord injury, traumatic spinal cord injury, alopecia, AlbS dementia, cerebral cord injury, traumatic spinal cord injury, alopecia, AlbS dementia, cerebral cord injury, traumatic spinal cord injury, alopecia, AlbS dementia, cerebral cord injury, and alopecia, and prosaposin receptor
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100.0%; Pred. No. 2.4e-40;
iive 0; Mismatches 0;
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Sequence 80 AA;

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The sequence represents human Saponin C (SapC), an essential co-factor for the lygosomal enzyme glucocerebrosidase, GCB. GCB is the enzyme involved in Gaucher's disease, a lygosomal storage disease. The invention relates to introducing new glycosylation sites into lysosomal enzymes/activators like GCB to improve their bioactivity. The novel enzymes/activators like GCB to improve their bioactivity. The novel epytypeptides are used for the prevention and treatment of Gaucher's disease, Parber's disease, Parber's disease, Sarber's disease, Shindler disease, Hunter syndrome, Sly syndrome, Hurler and Huler/Scheie syndromes
Example 5; Page 96; 97pp; English.
                                                                                                                                                                                                                                                                                                                               Sequence 80 AA;
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1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS Gaps ö 100.0%; Score 412; DB 4; Length 80; 100.0%; Pred. No. 2.4e-40; Live 0; Mismatches 0; Indels 80 61 ILLEEVSPELVCSMLHLCSG 80 61 ILLEEVSPELVCSMLHLCSG 80; Conservative Local Similarity Query Match Matches g ઠે

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9 9

> ABU62252 standard; protein; 80 AA (first entry) 29-AUG-2003 ABU62252; RESULT 4

Sphingolipid activator protein; saposin; neuroprotective; human; gene therapy; anionic phospholipid; fusogenic protein; prosaposin; Gauchers disease; saposin C. Sphingolipid activator protein C (saposin C)

Homo sapiens

US2003095999-A1. 22-MAY-2003. 09-FEB-2001; 2001US-00780438

11-FEB-2000; 2000US-0181754P

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oi x;

WPI; 2003-512933/48

Delivering pharmaceutical agent through membrane used for treating Gauchers disease, by applying composition comprising anionic phospholipids and fusogenic protein derived from prosaposin in carrier to Disclosure, Fig 4; 19pp, English. membrane

The invention describes a method of delivering a pharmaceutical agent through a membrane comprising applying to the membrane a composition (I) comprising: (1) anionic phospholipids; (2) a pharmaceutical agent contained within the phospholipids, and (3) a fusogenic protein or polypeptide derived from prosaposin in a carrier. The method can be used for delivering pharmaceutical agents through a biological membrane in cosmetic and medicinal applications, particularly for treating Gauchers disease. This is the amino acid sequence of sphingolipid activator protein C (saposin C) for use in the delivery composition 

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The invention relates to a prosaposin receptor agonist comprising a defined amino acid sequence of 14-50 amino acids conforming to the consensus sequence appearing as ADQ94330. The agonists are based on peptides derived from the C domain of human presaposin (or homologous peptides from other proteins). Also included are a pharmaceutical composition comprising the prosaposin receptor agonist in a pharmaceutical carrier, a method of alleviating neuropathic pain in a subject, a method of inhibiting neurite outgrowth (or inhibiting neural cell death, promoting myelination or inhibiting demyelination) and a cell death, promoting myelination or inhibiting demyelination) and a method of inhibiting sensory or motor neuropathy. The neuropathic pain cell from a peripheral nerve disorder, e.g. neuroma, nerve compression, nerve crush, nerve stretch and incomplete nerve compression, nerve crush, nerve stretch and incomplete nerve compression, neave crush, nerve stretch, and encomplete from a disorder of dorsal root ganglia, spinal cord, brainstem, thalamus, or cortex. The prosaposin receptor agonist, composition, and methods are useful in
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                                                                                                        1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSERCQEVVDTYGSSILS
                                                                               1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New prosaposin receptor agonist, useful in alleviating or treating
neuropathic pain, inhibiting the onset of neuropathic pain, neural cel
death, demyelination, or sensory or motor neuropathy, and stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, presaposin, C-domain, presaposin receptor agonist, neuropathic pain; neurite outgrowth, neural cell death; myelination, demyelination, neuropathy; peripheral nerve disorder; neuroma; nerve compression; nerve crush; nerve stretch; incomplete nerve transsection; mononeuropathy; polyneuropathy.
                                           ö
    Length 80;
                                           Indels
  Score 412; DB 7;
Pred. No. 2.4e-40;
                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, SEQ ID NO 24; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Human Presaposin protein, C-domain.
                                                                                                                                                                                                                                                                                                   ADQ94329 standard; protein; 80 AA.
                                                                                                                                                              80
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                                                                                                                                                                                 61 ILLEBVSPELVCSMLHLCSG
  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-00611307.
97WO-US004143.
97US-00928074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-DEC-2003; 2003US-00746442.
                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-2004 (first entry)
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-468194/44.
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurite outgrowth.
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    Ma.
Local S...
80;
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05-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O'brien JS;
                                                                                                                                                                                                                                                                                                                                             ADQ94329;
Query Match
                                       fatches
                                                                                                                                                                                                                                                                                   ADQ94329
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Length 80; Indele

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The subject is a mammal, preferably a human. The cell death preferably occurs through apoptosis. The agent is useful in treating cancer by inducing cell death in hyperproliferating cells. The present sequence represents a human Saposin C polypeptide.
                                                                                                                                                                                1 spuycevcertukkevtkiipninktekeii.parpkmcskipksiisecopevvotygssiis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pharmaceutical; neuropathy; analgesic; antidiabetic; cell death; diabetes; neurological disease; neuropathic pain; saposin C.
                                                                                                                100.0%; Score 412; DB 8;
100.0%; Pred. No. 2.4e-40;
                                                                                                                                                                                                                                                                                                                                             ADW80728 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human saposin C, SEQ ID NO:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-00611307.
97WO-US004143.
                                                                                                                                                                                                                                       61 ILLEBVSPELVCSMLHLCSG
                                                                                                                                                                                                                                                       61 ILLEBVSPELVCSMLHLCSG
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resulting from diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                      Best Local Similarity 100.
Matches 80; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 80 AA;
                                                                                            Sequence 80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-1996;
05-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6849602-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Obrien JS;
                                                                                                                                                                                                                                                                                                                                                                                  ADW80728;
                                                                                                                             Query Match
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ADW80728
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                          SKSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a agent comprising an inner leaflet component and a prosaposin-related polypeptide. The prosaposin-related polypeptide and a prosaposin-related polypeptide and a prosaposin-related polypeptide retains component is plasma-membrane affinity. The inner leaflet component is plasma-membrane affinity. The inner leaflet component is plasma-membrane affinity. The inner leaflet component in the agent promotes cell death in dislephatidylserine. The agent promotes cells of the agent can dislephatidylserine. The agent promotes cells of a subject; modulating be used in a method (M1) for modulating the distribution of an inner be used in a plasma membrane of a cell of a subject; modulating component in a pubject, treating (M3) cancer in a subject; modulation the plasma membrane is altered (preferably increased). The distribution the plasma membrane is altered (preferably increased). The distribution the plasma membrane is altered (preferably increased). The distribution the plasma membrane is altered (preferably selected from cells and cancer cells). In M2 and M3 the agent promotes cell (tumour cells and cancer cells). In M2 and M3 the agent promotes cell cancer in hyperproliferating cells which are preferably selected from sarccma, neuroblastoma, breast carcinoma, and squamous carcinoma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New agent comprising an inner leaflet component (preferably plasma phosphatidylserine) and a prosaposin-related polypeptide with plasma membrane affility comprising a sequence of 524 or 80 amino acids, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prosaposin; saposin C; phosphatidylserine; dioleoylphosphatidylserine;
cytostatic; apoptosis stimulator; human.
                              alleviating or treating neuropathic pain, inhibiting the onset of neuropathic pain, neural cell death, demyelination, or sensory or motor neuropathic pain, neimulating neurite outgrowth. The present sequence represents the C-domain of Human presaposin.
                                                                                                                                                                                                             1 SDYYCEVCEPLYKEYTKI. IDNNKTEKEILDAFDKMCSKL.PKSLSEBCCRVVDTYGSSILS
                                                                                                                                                                      Gaps
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0
                                                                                                                                         100.0%; Score 412; DB 8; Length 80;
100.0%; Pred. No. 2.4e-40;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 2; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                         ADU48631 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                   61 ILLEEVSPELVCSMLHLCSG 80
                                                                                                                                                                                                                                                                                            61 ILLEEVSPELVCSMLHLCSG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-2003; 2003US-0466166P.
16-MAR-2004; 2004US-00801517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Saposin C polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                         0uery Match
Best Local Similarity 100.
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004096159-A2.
                                                                                                                           Sequence 80 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                              ADU48631;
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The invention relates to pharmaceutical composition comprising a prosaposin receptor agonist and a carrier, where the composition is in a controlled release, liposomal or unit dosage form. The invention also controlled release, liposomal or unit dosage form. The invention also relates to prosaposin receptor agonists and the use of these agonists for myelinating neurite outgrowth, inhibiting neural demyelination and inhibiting sensory or myelination, inhibiting neural demyelination and inhibiting sensory or motor neuropathy. The pharmaceutical composition is useful for selevating neuropathy pain resulting from diabetes. The present sequence is human saposin C, which is derived from prosaposin. Note: The present sequence is given in the sequence listing, but is not further
New pharmaceutical composition comprising a prosaposin receptor agonist and a carrier, where the composition is in a controlled release, liposomal or unit dosage form, useful for alleviating neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 412; DB 9; Length 80;
Pred. No. 2.4e-40;
                                                                                                                                                                                                                                                     Disclosure, SEQ ID NO 24; 35pp; English.
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are sphingolipid activator proteins or coenzymes that also promotes acid beta-glucosidase activity by inducing the enzyme conformational change at acidic ph. The methods and composition of the invention are useful for enhancing the transport and delivery of pharmaceutical agents across and/or within dermal and mucosal membranes for both cosmetic and medicinal applications such as in treating Gaucher's disease. The present sequence is human saposin C fusogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Translational profiling, expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MTC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this
                                                                                                                                                                                                                                                                        SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma leukemia.
                                                                                                                                                                                                                                                   1 SDVYCEVCRFLVKEVTKLIDNNKTEKEILDARDKMCSKLPKSLSRECQEVVDTYGSSILS
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                                                                                                                                                                            ch 100.0%; Score 412; DB 9; Similarity 100.0%; Pred. No. 2.4e-40; 80; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human expressed protein tag (EPT) #1867.
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                                                                                                                                                                                                                                                                                                                         80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0316301P.
01-OCT-2001; 2001US-0336370P.
04-DBC-2002; 2002US-0358985P.
                                                                                                                                                                                                                                                                                                                      61 ILLEEVSPELVCSMLHLCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2002; 2002WO-US009671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tomlinson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-040607/03.
                                                                                                                                                                                                  Local Similarity
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                                                                                                                                               Sequence 80 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU05201;
                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to methods of delivering pharmaceutical agents across biological membranes where the pharmaceutical agent is contained within the phospholipid membrane and delivery is facilitated by a membrane fusogenic protein, saposin, derived from prosaposin. Saposins
                                       9
                                                                        9
                                                                                                                                                                                                                                                                                                                                                                     Saposin C; pharmaceutical; drug delivery; cosmetics; gauchers disease; metabolic; neurological disease; beta-glucosidase activator; sphingolipid activator protein.
                                                        SDVYCEVCEFLVKEVTKLIDININKTEKEILDAFDKWCSKLPKSLSEECQEVVDTYGSSILS
                                  SDVYCEVCEPLVKEVTKLIDNNKTEKRILDAPDKMCSKLPKSLSERCQEVVDTYGSSILS
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delivering a pharmaceutical agent through a dermal or mucosal mem
e.g. treat Gaucher's disease, comprises applying to the membrane
composition comprising a fusogenic protein, such as saposin C.
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te= "Beta-glucosidase activation region"
     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region"
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/note= "Neuritogenic region"
   Mismatches

    15
    note= "Lipid binding

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/note= "Lipid binding
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                                                                                                                                                                                                                                                                                                                                    Human saposin C fusogenic protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Helix 3"
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                                                                                                                                                                                                                               ADZ88479 standard, protein; 80
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                                                                                                                                                                                                                                                                                                    (first entry)
   Conservative
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Disulfide-bond
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Binding-site
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Best Local Similarity 100.
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 385 AA;
N-PSDB; ACC46687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; dithp; diagnostic and therapeutic polynuclectide; diagnosis; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; gastrointestinal disorder; transport disorder; neurological disorder; dastrointestinal disorder; transport disorder; nonective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; knock in; disease model; toxicological testing; transcript imaging;
                                                                                                                                                                                                                                                                                           ö
                                                                         myelona, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, myelona, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expessed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                          1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSISEGOEVVDTYGSSILS 60
                                                                                                                                                                                                                                                                                                                                               Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
Daughtery SC, Dam TC, Liu TP, Nguyen DA, Kleefeld Y, Geretin EH;
Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Plores V, Marwaha R, Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                               Gapa
       polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polymucleotides are particularly useful for treating or preventing
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                       100.0%; Score 412; DB 6; Length 210; 100.0%; Pred. No. 8.6e-40; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DITHP biochemical pathway protein.
                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR41750 standard; protein; 385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                      68 ILLEEVSPELVCSMLHLCSG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2001; 2011US-0280067P.
29-MAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-UUN-2001; 2001US-029428P.
20-JUN-2001; 2001US-0299428P.
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                                                                                                                                                                                                                                                                                                                                                                                                           61 ILLEEVSPELVCSMLHLCSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                      80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biochemical pathway
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                   Sequence 210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200297031-A2.
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ABR41750

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WPI; 2003-129518/12.

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The invention relates to novel human diagnostic and therapeutic computation relates to novel human diagnostic and therapeutic polymucleotides designated dithp (ACG46080-ACC46749) and to their encoded polymucleotide sequences at least 90% identical to the dithp CDNA polymucleotide sequences at least 90% identical to the dithp CDNA polymucleotide sequences at least 90% identical to the dithp cells and sequences of the invention; recombinant vectors, host cells and sequences; the transgenic organisms comprising dithp nucleic acid sequences; methods of proteins increarrays comprising dithp nucleic acid sequences; methods of proteins increarrays comprising dithp nucleic acid sequences; methods of correcting which specifically bind a DITMP protein and methods of describing dithp nucleic acid sequences; methods of correcting dithp nucleic acid sequences and DITMP proteins may be used in the probe. Dithp nucleic acid sequences and DITMP proteins may be used in the probe. Dithp nucleic acid sequences and DITMP proteins may be used to disorders; and connective tissue disorders; proliferative disorders; autoimmune or inflammatory disorders; bused to disorders; nad connective tissue disorders; proliferative disorders; proliferative disorders; proliferative disorders; proliferative disorders; proliferative disorders; proliferative and connective tissue disorders; gastroincestinal disorders; proliferative of protein activity or gene expression. DITMP screen for modulators of protein activity or gene expression of a tissue or encil type and to induce antibodies. They dithp nucleic acids are a source of antisense sequences, as a source of mentioned above, as a source of antisense sequence, as a source of mentioned above, as a source of antisense sequence, as a source of the generation of transgenic animal models of human disease or knock in the persent sequence represents a DITMP protein which is involved in a The present sequence represents a DITMP protein which is involved in a prochemical pathway. Note: The sequence for thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENSET; cytostatic; gene therapy; cancer; transgenic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 385;
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100.0%; Pred. No. 1.9e-39;
ive 0; Mismatches 0;
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                                                                                                                                                                                                              Claim 27; SEQ ID NO 1285; 591pp; English.
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17-JUL-2000; 2000WO-FR002057
                                                                   WPI; 2004-794441/78
    ESTE/) ESTELL D A.
              LYONS B H.
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 522 AA;
                          YAO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200105422-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                         (YAOJ/)
                                              Day AG,
               LYON/)
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Matches
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                                                                                                                                                                                                                                                                                                                        314 SDVYCEVCRFLVKEVTKLIDNNKTEKEILDAFDKWCSKLPKSLSEECQEVVDTYGSSILS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brain-associated disease; neuronal-associated disease; metabolic disorder; haematopoietic; cytostatic; immunosuppressive; cardiovascular; cerebroprotective; human; cysteine peptidase; enzyme; peripheral nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; Alzheimer's disease; Parkinson's disease; multiple sclerosis; sexual dysfuction; mood disorder; attention disorder; cypin; sexual dysfuction; mood disorder; attention disorder; hypotension; hypotenedon; psychotic disorder; neurological disorder; dyskinesia; organ transplant rejection.
                                                                                                                                                                                                                                                                                                              9
                                                                                                                                useful for preparing a composition for treating GENSET-
                                                                                                                                                                                    The invention relates to isolated GENSET polynuclectides and encoded polypeptides. The GENSET gene is useful for preparing a composition for treating GENSET-related disorders e.g., cancer. Sequences ABR39423-448 represent the novel GENSET polypeptide sequences
                                                                                                                                                                                                                                                                                                            1 SDVYCEVCEFLVKEVIKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protease; cancer; immune-related disorder; cardiovascular disease;
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                                                                                                                                                                                                                                                                ch 100.0%; Score 412; DB 6; Length 479; l Similarity 100.0%; Pred. No. 2.5e-39; 80; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258. .444 / note active domain
                                                                                                                                                                 Claim 2; Page 288-289; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cysteine peptidase enzyme #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADU24090 standard; protein; 522 AA
                                                                                                                                                                                                                                                                                                                                                                   374 ILLEEVSPELVCSMLHLCSG 393
                                                                                                                                                                                                                                                                                                                                                       61 ILLEEVSPELVCSMLHLCSG 80
10-AUG-2001; 2001US-0311305P.
24-AUG-2001; 2001US-0314734P.
07-SEP-2001; 2001US-0318204P.
01-OCT-2001; 2001US-0326470P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                           Tanaka H;
                                                                                                WPI; 2003-256539/25.
                                                                                                                                                                                                                                                                            Best Local Similarity
                                                     (GEST ) GENSET SA.
                                                                                                                                New GENSET gene, related disorders
                                                                                                             N-PSDB; ABZ76265.
                                                                                                                                                                                                                                            Sequence 479 AA;
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                                                                           Bejanin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADU24090;
                                                                                                                                                                                                                                                                 Query Match
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Domain
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
ADU24090
 a
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modulates the activity of a merical solution to the inversion traces.

Contacting step and determining whether test compound mediates the activity of the protease before and after contacting step and determining whether test compound modulates the extraction also relates to the proteins not previously identified as protease. The method is useful for identifying a compound that modulates the activity of a protease. It is useful for treating a disease or disorder e.g., cancer, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases or metabolic disorders (preferably cancer of tissue or haematopoietic crigin) in mammal, preferably human. The method is also useful for treating disease, of the peripheral nervous system, Alzhelmer's disease, whiltiple sclerosis, amyotrophic lateral sclerosis, viral infections caused by prions, infections caused by bacteria and fissues and disorders, pain, sexual dysfuction, mood disorders, advantances and disorders, contained and disorders, and diso
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                                                                                                                                                                                                                           Identifying compound that modulates activity of protease, by contacting protease with test compound, measuring activity of protease before and after contacting step, and determining whether test compound modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present sequence is the human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for identifying a compound that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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100.0%; Pred. No. 2.8e-39;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cysteine peptidase, a novel protease enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a human protein.
Yao J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 38; 206pp; English.
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Lyons EH,
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                                                                                                                                                                                                                                                                                                                                                                                                                              activity of protease
Estell DA,
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The present sequence represents a human protein, which is used in the method of the Invention. The specification describes a method which uses at least one polypeptide or polymucleotide sequence belonging to the cat least one polypeptide or polymucleotide sequence belonging to the parallel of the retinol-binding plasma protein, precursor of the ganglioside GMZ activator, calgranulin B or saposin B protein of families. The method is used for detecting, preventing or treating a companies, polymucleotides and polypeptides are used for diagnosis, prognosis, prevention and treatment of multiple solerosis (in its various forms and companies). They may also be useful in cases of e.g. Alzhaimer's and parkinson's diseases, amyotrophic lateral solerosis, rheumatoid pertenting expression of sense or antisense sequences). They can also be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 SDVYCEPLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS 60
                                                                                                                                      Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 412; DB 4; Length 523; 100.0%; Pred. No. 2.8e-39; Indel8 tive 0; Mismatches 0; Indel8
                                                                         Santoro L,
                                                                          Malcus C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human expressed protein tag (BPT) #1877.
                                                                                                                                                                                                                     Claim 1; Page 174-175; 209pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU05211 standard; protein; 523 AA.
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                                                                              Charles M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2002; 2002WO-US009671
       99FR-00009372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2003 (first entry)
                                         (INMR ) BIOMERIEUX STELHYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                  Ξ,
                                                                                                                    WPI; 2001-159475/16.
                                                                                    Kolbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200278524-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 523 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L0-OCT-2002
              15-JUL-1999;
                                                                                    Roecklin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU05211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
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The invention describes a purified polypeptide, which comprises a cramscription to kinase, phosphatase, protease, protease inhibitor, cramscription factor. The tramscription factor. The tramscription factor. The cramsporter, cytoskeletal protein, receptor or transcription factor. The cramsporter is useful as an immunogenic composition for eliciting in a polypeptide is useful as an immunogenic composition that pinds to the purified polypeptide, or the antibody that binds to this colypeptide, is useful for treating cancer. The polypeptide is also polypeptide, is useful for treating compounds that binds to a naturally processed class I MHC-binding polypeptide. The polypeptides and class I MHC-binding polypeptide. The polypeptides and polymucleotides are particularly useful for treating or preventing polymucleotides are particularly useful for treating or preventing compounds that binds are shown as are also useful for treating compounds that binds to screening agents for lymphoms or leukaemia. These are also useful for screening agents for captured above mentioned diseases. This sequence represents an treating the above mentioned diseases. This sequence for translational correction but was obtained in electronic format directly from WIPO at specification but was obtained in electronic format directly from WIPO at the printed profile to the printed profile pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAPDKMCSKLPKSLSEECOEVVDTYGSSILS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 412; DB 6; Length 523; 100.0%; Pred. No. 2.8e-39; Indels ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 1877; 134pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 ILLEEVSPELVCSMLHLCSG 389
                                                                                                                                     Urban RG
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01-0CT-2001; 2001US-0326370P.
04-DEC-2001; 2001US-0336780P.
20-FEB-2002; 2002US-0358985P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
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                                                                                                                                     Tomlinson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                  WPI; 2003-040607/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 523 AA;
                                                                                              (ZYCO-) ZYCOS INC
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30-AUG-1995
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                                                                                                                                             Chicz RM,
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Search completed: January 13, 2006, 16:30:19 Job time : 27.947 secs

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Query Match 100.0%; Score 412; DB 2; Length 524; Best Local Similarity 100.0%; Pred. No. 2.8e-39; Matches 80; Conservative 0; Mismatches 0; Indels 0

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Run on:

Sequence:

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Q99125 drosophila O5r848 pongo pygma O7pw6 anopheles g Q8n7t4 homo sapien O7pje6 anopheles g Q7pje7 anopheles g Q7pje7 anopheles g Q6nujl homo sapien Q4sj83 tetraodon n Q9ugj drosophila Q5bjn1 homo sapien O54pt7 dictyosteli Q8cln0 mus musculu Q8byv5 mus musculu Q8byv5 mus musculu Q8clc1 mus musculu
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A., Robo G., Han M., Wiemann S.;
Robo G., Golooofsta, 119-200, 239-318.
Robo G. (200006662; P.: Iping Metabolism; IEA.
Robo G. (200006662; P.: Iping Metabolism; IEA.
Robo G. (200006662; P.: Iping Metabolism; IEA.
Robo G. (200006662; P.: Robo G. (200006662; Robo G. (20006662; Robo G. (200006662; Robo G. (200006662; Robo G. (200006662); Robo G. (200006662; Robo G. (20006662; Robo G. (200006662; Robo G. (20000662; Robo G. (20000662
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Last annotation update)
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ilarity 100.0%; Pred. No. 2.2e-30;
Conservative 0; Mismatches 0;
                                       QSR848_PONPY
Q7PWG_ANOGA
Q08N74 HUMAN
Q7PJEG_ANOGA
Q7PJEG_ANOGA
Q7BJEG ANOGA
Q4SJ83_TETWG
Q4SJ83_TETWG
Q5BJJ1 HUMAN
Q58JJ1 HUMAN
Q58JJ1 HUMAN
Q58JJ1 HUMAN
Q68JZ0 MOUSE
Q0BJY5_MOUSE
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OSR406 PONPY PRELIMINARY;
AC OSR406.
DT 01-FEB-2005 (TrEMBLrel. 29, DT 01-FEB-2005)
CO NCBI_TAXID=9600;
RN (1)
RN (2000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000,
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TISSUE-Cortex;
The German cDNA Consortium;
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                                                                                                                                                                                                                                             January 13, 2006, 16:22:54; Search time 30.4636 Seconds (without alignments) 1852.779 Million cell updates/sec
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412
1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPELVCSMLHLCSG
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Compugen Ltd
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054037_HUMAN
058407_PONPY
058407_PONPY
05870 XENLA
048038_TETNG
081024_BRARE
069362_BRARE
069622_BRARE
069622_BRARE
0696426_XENLA
069734_RAT
06973_RAT
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OSJOJ6 HUMAN
OSNVDS PONPY
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OSD981 SCHJA
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                                   GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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RDert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;

RDert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;

RDert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;

Schoning of human full open reading frames in Gateway(TW) system entry vector (pDONR201).";

Vector (pDONR201).";

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleogtomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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NUCLEOTIDE 88321660; PubMed=2842863;
MEDLINE-88321660; PubMed=2842863;
O'Srien J.S., Kretz K.A., Dewji N., Wenger D.A., Esch F.,
Fluharty A.L.;
Fluharty A.L.;
"Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB-Liver;
MEDLINE-90129043; PubMed-2515150;
MEDLINE-90129043; PubMed-2515150;
MEDLINE-90129043; PubMed-2515150;

**Rorman E.G., Grabowski G.A.;

"Molecular cloning of a human co-beta-glucosidase cDNA; evidence that four sphingolipid hydrolase activator proteins are encoded by single genes in humans and rates.";

Genemics 5:486-492(1989).
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MEDITINE=89255151; PubMed=2498298;
MARANO T., Sandhoff K., Stuemper J., Christomanou H., Suzuki K.;
Makano T., Sandhoff K., Stuemper J., Christomanou H., Suzuki K.;
Structure of full-length cDNA coding for sulfatide activator, a Co-
beta-glucosidase and two other homologous proteins: two alternate
forms of the sulfatide activator.";
J. Blochem. 105:152-154(1989).
                                                              STANDARD; PRT; 524 AA.

SAP HUMAN STANDARD; PR538; P78541; P78546; P78547; P78558;

SOCIO 22; PO7292; P15793; P78538; P78541; P78546; P78547; P78558;

GEBG6; Q92739; Q92740; Q92741; Q92742;

GEBG6; Q92739; Q92740; Q92741; Q92742;

O1-APR-1998 (Rel. 07, Created)

O1-APR-1998 (Rel. 14, Last sequence update)

13-SEP-2005 (Rel. 48, Last annotation update)

13-SEP-2005 (Rel. 48, Last annotation update)

SAPOSTIN B-Val; SAPOSTIN B (Sphingolipid activator protein 1) (SAP-1)

SAPOSTIN B-Val; SAPOSTIN C (Co-beta-glucosidase) (Al activator)

(Glucosylceramidase activator) (Sphingolipid activator protein 2)

(SAP-2); SAPOSTIN D (Protein C) (Component C)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SAP-MU-0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=PSAP;
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MEDLINE=89207118; PubMed=3342555; Reunitzer G.; Kleinachmidt T., Christomanou H., Braunitzer G.; Complete amino-acid sequence of the naturally occurring A2 activator protein for enzymic aphingomyelin degradation: identity to the protein for enzymic aphingomyelin (SAP-1).";
                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 17-24; 165-172; 180-189 AND 298-302.

PREDLINE-93311991; PubMed-8323276; DOI=10.1006/abbi.1993.1328;

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Hiraiwa B.I., Martin B.M.;

"Isolation, characterization, and proteolysis of human prosaposin, the precureor of saposins (sphingolipid activator proteins).";

precureor Biochem. Blophys. 304:110-116(1993).
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"Nucleotide sequence of cloned cDNA for human sphingolipid activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of the sphingolipid activator protein-1 (SAP-1), the sulfatide sulfatase activator.";
                                                               NUCLECTIDE SEQUENCE OF 14-524.
MEDLINE=92307663; PubMed=1612590;
MEDLINE=92307663; PubMed=1612590;
Rorman E.G., Scheinker V., Grabowski G.A.;
Structure and evolution of the human prosaposin chromosomal gene.";
Genomics 13:312-318(1992).
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MEDLINE-93380576; PubMed-8370464; DOI=10.1016/0014-5793(93)80908-D;
MEDLINE-93380576; PubMed-8370464; DOI=10.1016/0014-5793(93)80908-D;
Tryynela J., Palmer D.N., Baumann M., Haltia M.;
"Storage of sapesins A and D in infantile neuronal ceroid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91192146; PubMed=2013321; DOI=10.1016/0014-5793(91)80308-P; Holtschmidt H.Y., Schnabel D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL PROTEIN SEQUENCE OF 60-142.
BEDLINE=89240739; PubMed=2717620;
Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S.,
Kishimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92068206; PubMed=1958198;
Kondoh K., Hineno T., Sano A., Kakimoto Y.;
"Isolation and characterization of prosaposin from human milk.";
Biochem. Biophys. Res. Commun. 181:286-292(1991).
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MEDLINE-86130593; PubMed=2666718;
Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,
Hill F., O'Brien J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The organization of the gene for the human cerebroside sulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osin A: second cerebrosidase activator protein.";
.. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).
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Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE OF 59-125 AND 304-513.
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MEDLINE=91006165; PubMed=2209618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88068647; Pubmed=2825202;
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same genetic locus.";
Science 241:1098-1101(1988).
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Name=PSAP; ÖRFNames=RP11-472K8.1-001;
Homo sapiens (Human).
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Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P.,
Stevens R.L., Fluharty C.B., Fluharty A.L.;
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                                                                         PROTEIN SEQUENCE OF 311-390.
MEDLINE=88163077; PubMed=3442600;
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Kleomschmidt amino-acid sequence and carbohydrate content of the
naturally occurring glucosylceramide activator protein (Al activator)
absent from a new human Gaucher disease variant.";
Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).
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Furst W., Schubert J., Machleidt W., Meyer H.E., Sandhoff K.;
"The complete amino-acid sequences of human ganglioside GM2 activator
protein and cerebroside sulfate activator protein.";
Nur. J. Biochem. 192:709-714(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89000190; PubMed=3048308;
Furst W., Machleidt W., Sandhoff K.;
"The precursor of sulfatide activator protein is processed to three different proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFIDE BONDS OF SAPOSINS B AND C, AND MASS SPECTROMETRY.
MEDLINE=55247790; PubMed=7730378; DOI=10.1074/jbc.270.17.9953;
Vaccaro A.M., Salvioll R., Barca A., Tattin M., Claffoni F., Maras 1 Siciliano R., Zappacosta F., Amoresano A., Pucci P.;
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                                                                                                                                                                                                                                                                                                               MEDLINE-89025876; PubMed-2845979;
Morimoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;
"Saposin D: a sphingomyelinase activator.";
Biochem. Biophys. Res. Commun. 156:403-410(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human urine.";
Genet. Metab. 68:391-403(1999).
                                                                                                                                                                                                                                                                                                   PARTIAL PROTEIN SEQUENCE OF 405-484.
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80; Conservative
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PRT;

Q53FJS HUMAN PRELIMINARY;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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TISSUE-Synovial membrane;
Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
"Construction and characterization of a full length-enriched and end-enriched cDNA library.";
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TISSUB-SYDOVIal membrane;
Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
Tanaka A., Yokoyama S.;
Tanaka A., Yokoyama S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AK223290; BAD97010.1; -; mRNA.
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10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Prosaposin (Variant Gaucher disease and variant metachromatic
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Prosaposin (Variant Gaucher disease and variant metachromatic
Homo sapiens (Human).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Fob G., Han M., Wiemann S.,
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR926102; CAI29728.1; -; mENA.
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            Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AL731541; CAI4087.1; -; Genomic_DNA. EMBL; AC06849; AAP35495.1; -; mRNA. EMBL; AC07370; CAI40837.1; JOINED, Genomic_DNA. GO; GO:0005764; C:1ysosome; IEA. GO; GO:0006629; P:1lpid metabolism; IEA. GO; GO:0006659; P:sphingolipid metabolism; IEA. GO; GO:0006665; P:sphingolipid metabolism; IEA. SGUENCE 524 AA; S8112 MM; 71977F7A8C9E1533 CRC64;
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SEQUENCE 527 AA; 58469 MW; 293FBB746C29C4D0 CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp459F0110.
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GO; GO:0005764; C:1yeosome; IEA.
GO; GO:0006629; P:1lpid metabolism; IEA.
GO; GO:0006655; P:sphingolipid metabolism; IEA.
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InterPro; IPR003119; SapA.
InterPro; IPR00136; SapB.1.
InterPro; IPR008130; SapB.2.
InterPro; IPR008130; SapGin.
InterPro; IPR008139; SapGin.
Pro; IPR008139; SapGin.
Pram; Pr05184; SapB.1; 4.
Pram; Pr05184; SapB.1; 4.
Pr078189; SapB.2; 4.
PrnTS; PR01797; SapB.2; 4.
ProDom; PR01732; SapB sub; 2.
SMART; SM0162; SAPA; 2.
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QSNVDS PONPY PRELIMINARY;
QSNVDS;
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Matches 80; Conservative
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317 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAPDKMCSKLPKSLSBECGEVVDTYGSSILS 376
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Name-PSAP; ORFNames=RP11-472K8.1-002;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
TISSUE=Brain;
TOTOK! Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama (Ohara O., Nagase T., Kikuno F.R.;
None Title.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL: AB209776; BAD93013.1; -; mRNA.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last samotation update)
Prosaposin (Variant Gaucher disease and variant metachromatic
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Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 80; Conservative 0; Mismatches 0; Indels (
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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EMBL, AC073370; CA140836.1; -; Genomic_DNA.
SNR; QSJQ371; 194-272, 311-390.
GO; GO:0005764; C:1ysosome; IEA.
GO; GO:0005659; P:1lpid metabolism; IEA.
GO; GO:006665; P:sphingolipid metabolism; IEA.
InterPro; IPR001119; SapA.:
InterPro; IPR001119; SapB.:
InterPro; IPR008138; SapB.:
InterPro; IPR008139; SapOsin.
InterPro; IPR008139; SapOsin.
InterPro; IPR008139; SapOsinB.
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374 ILLEEVSPELVCSMLHLCSG 393
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AC 055ENS HUMAN PRELIMINARY;

AC 10-MAY-2005 (TrEMBLrel. 30,

DT 10-MAY-2005 (TrEMBLrel. 30,

DT 10-MAY-2005 (TrEMBLrel. 30,

DT 10-MAY-2005 (TrEMBLrel. 30,

DT 10-MAY-2005 (TrEMBLrel. 30,

DE Prosaposin variant (Fragment GN Mame-prosaposin variant;

CN Name-prosaposin variant;

CN Mammalia; Eutheria; Euarchor oc Homo.

CN NCBL TaxID=9606;

RN (1]

RP TAXID=9606;

RN (1]

RP TOTOK! Y. TOYOGA A. Taked RA TOTOK! Y. TOYOGA A. TAKED S. TOTOK! Y. TOYOGA A. S. TOTOK! Y. TOYOGA A. S. TOTOK! Y. TOYOGA A. S. TOTOK! Y. TOWN TER.
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Q5JQ37;
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                                                                                                                                                              RESULT 6
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Matches
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                                                                                                                                                                                                                                                                                  311 SDVYCEVCEPLVKEVTKLIDNNKTEKEILDAPDKACSKLPKSLSEECOEVVDTYGSSILS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKWCSKLPKSPSEECQEVVDTYGSSILS 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                            SDVYCEVCEPLVXGVTKLIDNNKTEKEILDAPDKMCSKLPKSLSEECQEVVDTYGSSILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB-Cortex;
The German CDNA Consortium;
Bloecker H., Brandt P., Mewes H.W., Weil B., Amid C.,
Bloecker H., Ebocher M., Brandt P., Mewes H.W., Weil B., Amid C.,
Bloecker H., Eocher M., Wiemann S.;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
BRMB., CR861144; CAH93219.1; -; mRNA.
BRMB., CR861144; CAH93219.1; -; mRNA.
BRMB., CR861144; CAH93219.1; -; mRNA.
GO, GO:0005764; C1lysocome; IEA.
GO, GO:00056629; P:1ipid metabolism; IEA.
IN GO; GO:00066629; P:1ipid metabolism; IEA.
InterPro; IPR003119; SapB.
InterPro; IPR003119; SapB.
InterPro; IPR008139; SapGsin.
InterPro; IPR008139; SapGsin.
InterPro; IPR008140; SapB.
InterPro; IPR008139; SapGsin.
IPR mi; PF03199; SapB. 2; 4.
IPR mi; PF03199; SapB. 2; 4.
IPR MINTS; PR01797; SAPGSIN.
IPR MINTS; PR01797; SAPGSIN.
IPR MINTS; PR01797; SAPB. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAPDKMCSKLPKSLSEECQEVVDTYGSSILS
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                          Length 559;
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Pred. No. 1.2e-29;
0; Mismatches 1; Indels
                                                                                                                                                                                                                    Indels
                                                                                                                              559 AA; 61692 MW; 7C80741E6039AE38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58325 MW; CF3B146DDB6F5539 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp459J1314.
Name=DKFZp459J1314;
                                                                                                                                                                        Score 412; DB 2;
Pred. No. 2.7e-30;
                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      ILLEEVSPELVCSMLHLCSG 80
               Pfam; PP05184; SapB 1; 4.
Pfam; PP03489; SapB 2; 4.
Pfam; PP03489; SapB 2; 4.
ProDom; PD001732; SapB sub; 2.
SWART; SMO0162; SAPA; 2.
SEQUENCE 559 AA; 61692 MW; 7.
                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.3%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 PONPY
QER4U7 PONPY PRELIMINARY;
QSR4U7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similaria,
hes 79; Conservative
                                                                                                                                                                                                                  Conservative
Pfam; PF02199; SapA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 526 AA; 5
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                                                                                                                                                                                            Similarity
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                                                                                                                                                                   Query Match
Best Local Simil
Matches 80; C
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314 SDVYCEVCEPLVKEVTKLIDNNKTEKEILDTPDKWCSKLPKSLSERCQEVVDTYGSSILS 373
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AC P26779; Q9N2G4;

DT 01-MG4-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 47, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Proactivator polypeptide precursor [Contains: Saposin A (Protein A);

DE Saposin B (Sphingollipid activator protein 1) (SAF-1) (Cerebroside Be sulfate activator) (CSACt) (Dispersin) (Sulfatide/GM1 activator);

DE Saposin C (Co-beta-glucosidase) (Al activator) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D activator) (Component C)].
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                                                                   13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Brain cDNA, clone: QccE-13090, similar to human prosaposin (variant Gaucher disease and variantmetachromatic leukodystrophy) (PSAP),
(Brain cDNA, clone: QccE-13989, similar to human prosaposin (variant Gaucher disease and variantmetachromatic leukodystrophy)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   testis and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Obsda N., Hizter M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.; Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs."; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; ABL69527; BAE01735.1; "RNA.

EMBL; ABL69527; BAE0169.1; -; mRNA.

SEQUENCE 497 AA; 55306 MW; 4A1974FBDB883900 CRC64;
                                                                                                                                                                                                                                                                                                                                            Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;

Cercopithecidae, Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           International consortium for macaque cDNA sequencing, analysis; "DNA sequences of macaque genes expressed in brain or testis an evolutionary implications "; submitted (UUN-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 397; DB 2;
Pred. No. 6.3e-29;
          497 AA
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TISSUB-Mammary gland;
Azuma N., Yoshida K.;
"RT-PCR cloning of bovine prosaposin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 ILLQEVSPELVCSMLRLCSG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILLEEVSPELVCSMLHLCSG 80
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NCBI_TaxID=9913;
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Q4R590 MACFA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 96.2
nes 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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367 3
525 AA;
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                                                                                                              DOMAIN
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                                                                                       TISSUE-SPICENT.

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A Sano A., Mizuno T., Kondoh K., Hineno T., Ueno S.-I., Kakimoto Y.,

Sano A., Mizuno T., Kondoh K., Hineno T., Ueno S.-I., Kakimoto Y.,

Sano A., Mizuno T., Kondoh K., Hineno T., Ueno S.-I., Kakimoto Y.,

A Morita N.;

In Saposin-C from bovine spleen; complete amino acid sequence and

relation between the structure and its biological activity.";

Telation between the structure and its biological activity.";

Biochin. Biophys. Acta 1120:75-80(1992).

The sponential action of specific hydrolases. Some of these

by the sequential action of specific hydrolases. Some of these

c enzymes require specific low-molecular mass, non-enzymic proteins:

the sphingolipids activator proteins (coproteins) (By similarity).

the sphingolipids activator proteins (coproteins) (By similarity).

C elucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and

galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).

C saposin C apparently acts by combining with the enzyme and acidic

c lipid to form an activated complex, rather than by solubilizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR SHR; P26779; 195-273, 312-390.

DR SHR; P26779; 195-273, 312-390.

DR InterPro; IPR003109; SapA.

DR InterPro; IPR003119; SapB.

DR InterPro; IPR008139; SapD.

DR InterPro; IPR008139; SapD.

DR InterPro; IPR008139; SapD.

DR InterPro; IPR008137; Surfactant_B.

DR Ffam; PF02199; SapB.

DR Ffam; PF02189; SapB.

DR PR03719; SapD.

DR PR03718; PS01109; SapB.

DR PR03718; PS51110; SaPB.

DR PR03718; PS51010; SAP.

DR PR03718; PS50115; SAP.

DR PR03718; PS50115; SAP.

DR PR03718; PS50110; PS50110; SAP.

DR PR03718; PS50110; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the substrate.

--- FUNCTION: Saposin B stimulates the hydrolysis of galacto-cerboside sulfate by arylaulfatase A (EC 3.1.6.8), GM1. cerebroside sulfate by larylaulfatase A (EC 3.2.1.23) and gangliosides by beta-galactosidase (EC 3.2.1.23) and gangliosides by beta-galactosidase A (EC 3.2.1.22). globotriaosylecramide by alpha-galactosidase A (EC 3.2.1.22). sphingolipid hydrolases (By similarity).

--- FUNCTION: Saposin B is a specific sphingomyelin phosphodiesterase activator (EC 3.1.4.12) (By similarity).

--- SUBCELLULAR LOCATION: Lysosomal.

--- SUBCELLULAR LOCATION: Lysosomal.

--- PTM: This precursor is proteolytically processed to 4 small peptides, which are similar to each other and are sphingolipid pydrolase activator proteins (By similarity).

C--- SIMILARITY: Contains 2 saposin A-type domains.

--- SIMILARITY: Contains 4 saposin B-type domains.
              Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saposin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saposin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saposin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB036791; BAA95677.1; -; mRNA.
HSSP; Q92739; IM12.
                                                                                 PROTEIN SEQUENCE OF 312-391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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Sano A., Radin N.S., Johnson L.L., Tarr G.E.;
The activator protein for glucosylceramide beta-glucosidase from guinea pig liver. Improved isolation method and complete amino acid sequence.";
J. Biol. Chem. 263:19597-19601 (1988).
Saposin A and saposin C atimonale by beta-galactosylceramidase (EC 3.2.1.45).
Galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).
Saposin C apparently acts by combining with the enzyme and acidic saposin C apparently acts by combining with the proposition of the proposition of the complex of the complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SDVYCEVÇEFLAKEVIKLIDNNKTEKEILDAFDKMCSKLPKSLSEEÇQEVVDTYGSSILS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;

Hystricognathi; Cavildae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .) (Potential).
.) (Potential).
.) (Potential).
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01-FEB-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Saposin C (CO-beta-glucosidase) (Glucosylceramidase activator)
Sphingolipid activator protein 2) (SAP-2).
Name=PSAP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293AFCOFB9C4FA99 CRC64;
                                                                                                                Saposin A-type 1.
Saposin B-type 2.
Saposin B-type 3.
Saposin B-type 3.
Saposin B-type 3.
Saposin B-type 4.
Saposin B-type 3.
N-linked (GLONAC.)
N
Saposin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89066787; PubMed=3198642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 ILLDEASPELVCSMLHLCS 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ILLEEVSPELVCSMLHLCS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58120 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   initiative.";
                                                                                                                                                                                                                                                                                                  TISSUE=Whole;
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                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A villalon D.K., Muzny D.M., Maden A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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01-0cr-2003 (TrEMBLrel. 25, Last sequence update)
01-0cr-2004 (TrEMBLrel. 26, Last annotation update)
MGC64541 protein.
MGC64541 protein.
Manopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Annra; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1797; SAFOSIN.
PRODOM; PRO1797; SAFOSIN.
PRODOM; PRO0741; SapB; 1.
SMART; SM00741; SapB; 1.
BROSTTE; PS50015; SAP B; 1.
Direct protein sequencing; Glycoprotein; Lipid metabolism; Sphingolipid netabolism.
Saphingolipid netabolism.
Saposin B-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.3%; Score 261; DB 1; Length 81; 61.8%; Pred. No. 6.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saposin B-type.
N-linked (GlcNac. .).
By similarity.
By similarity.
By similarity.
E564CE1F0A292596 CRC64;
the substrate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 61.8%; Pred. No. 6.3e-
Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                            HSSP; Q92739; IMI2.
InterPro; IRR007856; SapB 1.
InterPro; IRR008138; SapB 2.
InterPro; IRR008140; SapB 80b.
InterPro; IRR008131; Saposin.
InterPro; IRR008139; SaposinB.
Pfam; PPO5184; SapB 1; 1.
Pfam; PPO3489; SapB 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEEVSPELVCSMLHLC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7SY70 XENLA PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AA;
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DISULFID
SEQUENCE
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299 NNVYCEVCELMISQIEKLIDNNRTRENIKQSLEKVCKLIPSQYTQKCEDIIDEYCDPLIE 358
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota, Meopterygii, Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                             MEDLINE-22341132; PubMed-12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Whole;
KIdin S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054988; AAH54988.1; -; mRNA.
HSSP; Q92739; 1M12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-5EP-2005 (TrEMBLrel. 31, Created)
13-5EP-2005 (TrEMBLrel. 31, Last sequence update)
13-5EP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 17 SCAPI5006, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57555 MW; 57CFA5E2093F6FB1 CRC64;
                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005764; C:lysosome; IEA.
GO; GO:0006629; P:lipid metabolism; IEA.
GO; GO:0006665; P:sphingolipid metabolism; IEA.
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InterPro; IPR007856; SapB 1.
InterPro; IPR008138; SapB 2.
InterPro; IPR008140; SapB sub.
InterPro; IPR008139; Saposin.
InterPro; IPR008139; SaposinB.
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ProDom; PD001732; SapB sub; 2.
SMART; SM00162; SAPA; Z.
SMART; SM00741; SapB; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dev. Dyn. 225:384-391(2002).
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Pfam; PF05184; SapB 1; 4.
Pfam; PF03489; SapB 2; 4.
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A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
A Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Iutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
The early vertebrate proto-karyotype.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 FCAICEAVMKQLEAMLEDKTTEEEVIHAVEKVCSYLPSSMSSQCKDLVEAYGEAIIDLLV 398
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FRB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Match 50.2%; Score 207; DB 2; Length 55 Local Similarity 39.0%; Pred. No. 5e-11; les 30; Conservative 30; Mismatches 17; Indels
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NON TER 550 550
SEQUENCE 550 AA; 60620 MW; 30FABFA766357628 CRC64;
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Ensembl, ENSPAGGOODO013968; Danio rerio.
Ensembl, ENSPAGGOODO013968; Danio rerio.
Ensembl, ENSPAGGOODO013968; Danio rerio.
GO; GO:0005764; C:1y8080me; IEA.
GO; GO:0006629; P:1lpid metabolism; IEA.
GO; GO:0007885; P:respiratory gaseous exchange; IEA.
GO; GO:0006665; P:sphingolipid metabolism; IEA.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Lysosomat cofactor/neurotrophic factor prosaposin.
Name=psap;
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InterPro; IPR008137; Surfactant_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 QQVDPKTVCTMLALCNG 415
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InterPro; IPR007856; SapB 1.
InterPro; IPR008138; SapB 2.
InterPro; IPR008140; SapB sub.
InterPro; IPR008373; Saposin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 EEVSPELVCSMLHLCSG 80
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QBUVZ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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Pfam: PF02199; SapA; 2.

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TISSUE-Whole;

MEDLINE-2236257;

MEDLINE-2236257;

MEDLINE-2236257;

MEDLINE-2236257;

MEDLINE-2236257;

MEDLINE-2236257;

MEDLINE-2236257;

MEDRINE-2236257;

MISCAUL S.F., Zecherg B., Buttow K.H., Schaefer C.F., Bhat N.K.,

A Alschul S.F., Zecherg B., Buttow K.H., Schaefer C.F., Bhat N.K.,

A Alschul S.F., Zecherg B., Buttow K.H., Schaefer C.F., Bhat N.K.,

A Alschul S.F., Zecherg B., Buttow K.H., Schaefer C.F., Bhat N.K.,

A Alschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Bacheron M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.H., Peters G.J., Abramson R.D., Mullahy S.J.,

Boak S.A., McEwan P.J., McKernan K.J., Malek J.H., Rulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergien E.J., Lu X., Gibbs R.A.,

Rahakesley K.W., Touchman M., Madan A., Rodrigues S., Sanchez A.,

Rahakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Schenk R.W.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Schnertion M.C., Marra M.A.;

Schnertion M.S., Schent J.E., Jones S.J.M., Marra M.A.;

Schnertion M.C., Grimwood J., Schmutz M.C., Smallus D.E.,

Schnertion M.C., Schent J.E., Jones S.J.M., Marra M.A.;

Schnertion M.S., Schein J.E., Jones S.J.M., Marra M.A.;

Schnertion M.S., Schein J.E., Jones S.J.M., Marra M.A.;
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Cyprinidae; Danio.
NCBI_TaxID=7955;
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TISSUB=Whole;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063994; AAH63994.1; -; mRNA.
EMBL; BC063994; AAH63994.1; -; mRNA.
EMBL; BC063994; P. 11pid metabolism; IEA.
GO; GO:0006569; P. 11pid metabolism; IEA.
GO; GO:0006665; P. Pespiratory gaseous exchange; IEA.
GO; GO:0006665; P. Sphingolipid metabolism; IEA.
InterPro; IPR007856; SapA.
InterPro; IPR007856; SapA.
                                                                                                                                                                                                                                                                                                                                                                                            520 AA; 57431 MW; P9E620F84BA41CB5 CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pfam; PF05184; SapB_1; 3.
Pfam; PF03489; SapB_2; 4.
PRINTS; PR01797; SAPDSIN.
ProDom; PD0001732; SapB_sub; 2.
ProDom; PD008002; Surfactant_B; 1.
SWART; SM00162; SAPB; 2.
SWART; SM00741; SapB; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEP3G7_BRARE PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prosaposin.
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O6P3GT
D1 O6P3GT
D2 O6P3GT
D2 O6P3GT
D2 O6P3GT
D3 O5-JU
D1 O5-JU
D2 O6P3GGT
D3 O6P3GGT
D3 O6P3GGT
D4 O6P3GGT
D5 O7D
D6 O6P3GGT
D6 O6P3GGT
D6 O6P3GGT
D6 O6P3GGT
D6 O6P3GT
D7 O6P3GT
D6 O6P
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Wed Jan 18 11:58:43 2006
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49.8%; Score 205; DB 2; Length 520;
Best Local Similarity 40.8%; Pred. No. 7.3e-11;
Matches 31; Conservative 26; Mismatches 19; Indels 0; Gaps
R InterPro; IPR008138; SapB 2.
R InterPro; IPR008140; SapB = ub.
R InterPro; IPR008137; Saposin.
R InterPro; IPR008137; SaposinB.
R InterPro; IPR008137; Surfactant_B.
R Pfam; PF02189; SapB 1; 3.
R Pfam; PF03189; SapB 2; 4.
R PRINTS; PR01777; SAPOSIN.
R PRODOM; PD0010722; SapB = ub; 2.
R ProDom; PD0080022; Surfactant_B; 1.
R ProDom; PD0080022; Surfactant_B; 1.
SMART; SM00162; SAPA; 2.
SEQUENCE : 520 AA; 57444 MW; 91D35DB81A1ED6DC CRC64;
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Search completed: January 13, 2006, 16:34:22 Job time : 31.4636 secs

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Sequence 3, Application US/09753126
Patent No. US20020127219A1
GENERAL INFORMATION:
APPLICANT: OKKELS, JENS SIGURD
APPLICANT: JENSEN, ANNE DAM
APPLICANT: HALKIER, TORBEN
APPLICANT: HALKIER, TORBEN
APPLICANT: HALKIER, TORBEN
APPLICANT: HALKIER, TORBEN
APPLICANT: HALKIER, BOLDING
TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES
TITLE OF INVENTION: ACTIVATORS
FILE REPERENCE: 31-0006600US
CURRENT APPLICATION NUMBER: US/09/753,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-767-007A-3
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38, Appl
2, Appli
1877, Ap
60, Appl
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386, App
1207, Ap
23, Appl
56, Appl
1, Appli
                                                                                                     January 13, 2006, 16:26:40; Search time 15.2318 Seconds (without alignments) 2194.512 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-110-801-517-2
US-110-801-517-2
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US-10-473-127-1867
US-09-978-418-40
US-10-465-231-40
US-09-767-0078-2
US-10-473-127-1877
US-09-751-708A-60
US-09-751-708A-60
US-09-751-708A-60
US-09-751-708A-60
US-10-46-442-23
US-10-408-7553-1207
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US-10-413-127-1865
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US-10-473-127-1874
US-10-473-127-1878
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US-09-753-126-3
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Maximum DB
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Sequence 3, Application US/09767007A
; Sequence 3, Application US/09767007A
; Patent No. US20020077275A1
; GRENRAL INFORMATION:
   APPLICANT: John S. O'Brien
; APPLICANT: John S. O'Brien
; APPLICANT: John S. O'Brien
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREPROM
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREPROM
; FILE REFERENCE: MYELOS.2DC1C.
; CURRENT APPLICATION NUMBER: US/09/767,007A
; CURRENT APPLICATION NUMBER: 08/958,970
; PRIOR FILING DATE: 1997-10-08/
; RIOR FILING DATE: 1997-10-08/
; SEQ ID NO 3; SEQ ID NO 3
; LENGTH: 80
                                                                                                                23, Appl
1875, Ap
61, Appl
61, Appl
73, Appl
57, Appl
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US-10-473-127-1879
US-10-473-127-1880
US-10-473-127-1881
US-10-473-127-1881
US-10-473-127-2041
US-11-036-687-23
US-10-473-127-1875
US-09-870-759-61
US-09-751-768-61
US-10-428-817A-57
US-110-473-127-1876
US-10-473-127-1876
US-10-473-137-137-1876
US-10-473-137-137-1876
US-10-473-137-137-1876
US-10-473-137-137-1876
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TYPE: PRT
ORGANISM: Homo sapiens
Query Match
Best Local Similarity
Matches 80; Conserva
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Sequence 3, Application US/10330697
Publication No. US20040009165A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JUNEAR SIGURD
APPLICANT: HALKIEK, TORBEN
APPLICANT: HALKIEK, TORBEN
TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYME
TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYME
TITLE OF INVENTION: ACTIVATORS
TITLE OF INVENTION: ACTIVATORS
TITLE OF INVENTION: ACTIVATORS
TITLE OF INVENTION: ACTIVATORS
FILE OF INVENTION: MUMBER: US/10/330,697
CURRENT APPLICATION NUMBER: US/09/753,126
PRIOR PILING DATE: 2000-16-11
PRIOR FILING DATE: 2000-16-12
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-06-12
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           CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: PA 1999 01891
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 60/174,652
PRIOR PILING DATE: 2000-01-06
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-13
PRIOR PILING DATE: 2000-07-11
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 3
LENGTH: 80
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 80
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Best Local Similarity 100.0
Matches 80; Conservative
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US-09-753-126-3
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US-10-330-697-3
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                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/10746442

Sequence 24, Application US/10746442

PUBLICANTON US20040121958A1

GENERAL INFORMATION:

APPLICANT: O'Brien, John S.

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/746,442

CURRENT APPLICATION NUMBER: 2003-12-24

CURRENT APPLICATION NUMBER: APPLICATION NUMBER: US/08/928,074

PRIOR PILING DATE: FILING DATE: 1997-09-11

PRIOR PILING DATE: FILING DATE: 1996-03-05

PRIOR PELING DATE: FILING DATE: 1996-03-05

PRIOR FILING DATE: FILING DATE: 1996-03-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0

LENOTH: 80
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61 ILLEEVSPELVCSMLHLCSG 80
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US-10-801-517-2

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8 SDVYCEVCEPLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEKCOEVVDTYGSSILS 67
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| Sequence 40. Application US/09978418
| Publication No. US20030118997A1
| GENERAL INFORMATION:
| APPLICANT: Belanin, Stephan
| APPLICANT: Belanin, Stephan
| TITLE OP INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
| FILE REPERENCE: 142.USS. REG
| TITLE OP INVENTION: HUMBER: US/09/978,418
| CURRENT APPLICATION NUMBER: US/09/978,418
| CURRENT PILING DATE: 2002-10-15
| PRIOR PILING DATE: 2001-0-16
| PRIOR PILING DATE: 2001-0-8-10
| PRIOR PILING DATE: 2001-0-0-10
| PRIOR PILING DATE: 2001-0-0-0
| PRIOR PILING DATE: 2001-09-07
| PRIOR PILING DATE: 2001-09-07
| PRIOR PILING DATE: 2001-10-01
| PRIOR PILING DATE: 2001-10-01
| NUMBER OF SEQ ID NOS: 52
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Pred. No. 7.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 412; DB 5; 100.0%; Pred. No. 2.8e-36;
                                                                                                                            TITLE OF INVENTION: TRANSLATIONAL PROFILING FILE REFERENCE: 08191-026WOI CURRENT APPLICATION NUMBER: US/10/473,127 CURRENT FILING DATE: 2003-09-26 PRIOR APPLICATION NUMBER: 60/279,495 PRIOR APPLICATION NUMBER: 60/295,544 PRIOR APPLICATION NUMBER: 60/292,544 PRIOR PILING DATE: 2001-03-28 PRIOR APPLICATION NUMBER: 60/326,370 PRIOR PILING DATE: 2001-08-08 PRIOR APPLICATION NUMBER: 60/326,370 PRIOR PILING DATE: 2001-10-01 PRIOR APPLICATION NUMBER: 60/336,370 PRIOR PILING DATE: 2001-10-04 PRIOR PILING DATE: 2001-12-04 PRIOR FILING DATE: 2001-02-20 NUMBER OF SEQ ID NOS: 2041 SOFTWARE: PARESRO FOR WINDOWS VERBION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                   ; Sequence 1867, Application US/10473127; Publication No. US20040236091A1; GENERAL INFORMATION: APPLICANT: Zycos Inc.
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US-10-473-127-1867
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 80; Conserval
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Best Local Similarity
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LENGTH: 479
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                                                                                                                                               1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS 60
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                                                                                                            1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS
                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/11036867
Publication No. US20050164948A1
GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSERE: 1918 & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                              ö
          Length 80;
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                                                           0; Indels
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ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPUTED:
COMPUTER: IBM COMPATIBLE
APPLICATION NUMBER: US/08/928,074
FILING DATE: 11-SEP-1997
APPLICATION NUMBER: 08/611,307
FILING DATE: 05-MAR-1996
APPLICATION NUMBER: PCT/US97/04143
FILING DATE: 05-MAR-1996
APPLICATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
TELEPHONE: 619/678-5070
        ; Score 412; DB 5;
; Pred. No. 8.4e-37;
0; Mismatches 0;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                   61 ILLEBVSPELVCSMLHLCSG 80
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        100.0%;
Query Match 100.0
Best Local Similarity 100.0
Matches 80; Conservative
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US-09-767-007A-2
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              Query Match
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US-10-485-231-40

Sequence 40, Application US/10485231

Publication No. US20050119171A1

GENERAL INFORMATION:
TILE OF INVENTION:
FILE REFERENCE: 142.W01

FILE REFERENCE: 142.W01

CURRENT FILING DATE: 2004-01-29

PRIOR FILING DATE: 2004-01-29

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-24

SOFTWARE: 479

SOFTWARE: 479

LENGTH: 479
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                                        1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDT
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Best Local Similarity 100.0%; Score 412; DB 5; Length 479;
Best Local Similarity 100.0%; Pred. No. 7.88-36;
Matches 80; Conservative 0; Mismatches 0; Indels
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Sequence 38, Application US/10618281
Sequence 38, Application US/10618281
Publication No. US20040219609A1
GENERAL INFORMATION:
APPLICANT: Day, Anchory G.
APPLICANT: Batell, David A.
APPLICANT: Estell, David A.
APPLICANT: Bric H.
APPLICANT: Wao, Jian
TITLE OF INVENTION: Methods for Modulating Proteins Not
TITLE OF INVENTION: Previously Known as Proteases
FILE REFERENCE: GC773-2
CURRENT APPLICATION NUMBER: US/10/618,281
CURRENT APPLICATION NUMBER: US 60/395,325
PRIOR APPLICATION NUMBER: US 60/395,325
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 92
NUMBER OF SEQ ID NOS: 92
      Indels
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          0; Mismatches
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                                                                                                                                                  374 ILLEEVSPELVCSMLHLCSG 393
                                                                                                                          61 ILLEEVSPELVCSMLHLCSG 80
              80; Conservative
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; ORGANISM: Homo sapiens
US-10-618-281-38
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LENGTH: 522
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Sequence 2, Application US/09767007A
; Sequence 2, Application US/09767007A
; Patent No. US2002007275A1
; Patent No. US2002007075A1
; GENERAL INFORMATION:
APPLICANT: John S. O'Brien
APPLICANT: John S. O'Brien
TITLE OF INVENTION: PARMACEUTICAL COMPOSITIONS COMPRISING
TITLE OF INVENTION: PARMACEUTICAL AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM
TITLE OF INVENTION: PARMACEUTICAL SUBJOINT
FILE REPREDACE: MYELOS. 2001-01-22
CURRENT FILING DATE: 2001-01-22
PRIOR PILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SOFTWARE: PARMACEUTICAL SUBJOINT S
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Length 522
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100.0%; Pred. No. 8.7e-36;
ative 0; Mismatches 0;
100.0%; Score 412; DB 5;
illarity 100.0%; Pred. No. 8.6e-36;
Conservative 0; Mismatches 0;
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US-10-473-127-1877

Sequence 1877, Application US/10473127

Publication No. US20040236091A1

GENERAL INFORMATION:

APPLICANT: Zycos Inc.

TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REPERENCE: 08191-026W01

CURRENT APPLICATION NUMBER: US/10/473,127

CURRENT FILING DATE: 2003-09-26

PRIOR APPLICATION NUMBER: 60/279,495

PRIOR PILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-03-28

PRIOR PILING DATE: 2001-05-21

PRIOR PLING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: 60/326,370

PRIOR PILING DATE: 2001-10-01

PRIOR PILING DATE: 2002-02-00
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SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 80; Conservative
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                                                      Best Local Similarity
Matches 80; Conserva
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Best Local Similarity 100.0%; Pred. No. 8.7e-36; Matches 80; Conservative 0; Mismatches 0;
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Job time : 15.2318 secs
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Best Local Similarity
Matches 80; Conserval
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US-10-267-502-386
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LENGTH: 524
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Patent No. US20020177551A1
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60, Application US/09751708A
Publication No. US20030157113A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT PAPLICATION UNMBER: US/09/751,708A
CURRENT FILING DATE: 1999-12-28
FRIOR RILING DATE: 1999-12-28
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                                                                                                                                                                                                                      1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS 60
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                                                                                                                               Query Match
100.0%; Score 412; DB 5; Length 523;
Best Local Similarity 100.0%; Pred. No. 8.7e-36;
Matches 80; Conservative 0; Mismatches 0; Indels
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SOFWARE: Patentin version 3.1
SEQ ID NO 60
ENOTH: 524
                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-473-127-1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CAGANISM: Homo sapiens
US-09-870-759-60
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ORGANISM: Homo sapiens
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US-09-751-708A-60
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SEQ ID NO 1877
LENGTH: 523
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                                       1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS
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Pred. No. 8.7e-36;
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100.0%; Pred. No. e...
0; Mismatches
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Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Kim, Jaeseob
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT PILING DATE: 2003-01-27
WUMBER OF SEQ ID NOS: 439
SOFTWARE: PatentIn version 3.2
                                                                                                                                                 371 ILLERVSPELVCSMLHLCSG 390
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US-10-267-502-386
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sequence 949, App Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 106, App Sequence 106, App Sequence 132, App Sequence 1447, Ap Sequence 2172, Ap Sequence 2172, Ap Sequence 2172, Ap Sequence 256, Ap Sequence 256, Ap Sequence 256, App Sequence 256, App

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Sequence 1631, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Adarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom

ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR PILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PE SEQ_genes Version 1.0

SEQ ID NO 1631

LENGTH: 524
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Publication No. US20050282755A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HARIN
APPLICANT: ARIN
APPLICANT: MACHIBIDT, THOMAS
APPLICANT: SCOUGH, DATID
APPLICANT: CONGER, DES
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
TITLE OF INVENTION: THEREOF
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US-10-636-320-6
US-10-763-712A-166
US-11-089-551A-30
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US-11-089-551A-30
US-11-089-551A-30
US-11-087-550-81
US-10-821-234-1456
US-11-08-55-500-81
US-10-467-657-2566
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100.0%; Pred. No. 7.7e-38;
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Best Local Similarity 100.0
Watches 80; Conservative
  TYPE: PRT
CORGANISM: Homo sapiens
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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-467-657-5296

US-11-124-368A-280

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APPLICANT: ALMET, SCOTT A.
APPLICANT: ZEH, KARIN
APPLICANT: STOLOW, DAVID
APPLICANT: STOLOW, DAVID
APPLICANT: CONGER, DE
APPLICANT: CONGER, DE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION NUMBER: US/11/078,469
FILE REFERENCE: ANS-2001-UT
CURRENT FILING DATE: 2005-03-11
PRIOR PELLOGATION NUMBER: 60/54,526
PRIOR PELLOGATION NUMBER: 60/549,526
PRIOR FILING DATE: 2004-03-18
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
NUMBER OF SEQ ID NOS: 294
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Best Local Similarity 21.1%; Pred. No. 0.43;
Matches 15; Conservative 21; Mismatches 34; Indels
                                                                                                                                                                                                                                                                          17.1%; Score 70.5; DB 7; Length 129; 21.1%; Pred. No. 0.31; tive 21; Mismatches 34; Indels
FILE REPERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT FILING DATE: 2005-03-11
PRIOR PELLING DATE: 2004-03-18
PRIOR PILLING DATE: 2004-03-18
PRIOR PILLING DATE: 2004-10-15
NUMBER OF SECULIN NOS: 294
SOFTWARE: PACENTIN Ver. 3.3
SEQ ID NO 20
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US-11-196-400-3
US-11-196-400-3
Sequence 3, Application US/11196400
Publication No. US20050287166A1
GENERAL INFORMATION:
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US-11-078-469-22
Sequence 22, Application US/11078469
Bublication No. US20050282755A1
GENERAL INFORMATION
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Best Local Similarity 21.1%
Matches 15; Conservative
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ORGANISM: Homo sapiens
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US-11-078-469-21
US-11-078-469-21

y Bublication No. US20502082755A1

y Publication No. US20502082755A1

y Publication No. US20502082755A1

y APPLICANT: HART, SCOTT A.

y APPLICANT: STOLOW, DAVID

y APPLICANT: CONGER, DE

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: UNDER: US/11/078,469

CURRENT FILING DATE: 2005-03-11

PRIOR FILING DATE: 2004-03-18

PRIOR FILING DATE: 2004-03-18

PRIOR FILING DATE: 2004-03-18

PRIOR FILING DATE: 2004-10-15

NUMBER OF SEQ ID NOS: 294

SOFTWARE PARENTED NOS: 294
APPLICANT: DAUBERSIES, FIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE STERRENCE: 2007-3180DLV
CURRENT APPLICATION NUMBER: US/09/742,096
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 1998-02-06
PRIOR PILING DATE: 1998-02-06
PRIOR PILING DATE: 1998-02-06
PRIOR PILING DATE: 1996-06-13
PRIOR PILING DATE: 1996-06-13
PRIOR FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENT OF SEQ ID NOS: 29
SEQ ID NO 3: 550 ID NO 
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Best Local Similarity 25.0%; Pred. No. 8.3;
Matches 15; Conservative 21; Mismatches
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US-11-196-400-3
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Best Local Similarity
Matches 15; Conserva
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APPLICANT: MONACI Elisabetta
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR PLING DATE: 2003-04-07
PRIOR PLING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 975
LENGTH: 989
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15.5%; Score 64; DB 6; Length 476;
Best Local Similarity 31.7%; Pred. No. 7.6;
Matches 19; Conservative 10; Mismatches 19; Indels
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26.0%; Pred. No. 14;
tive 16; Mismatches 31; Indels
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DATABASE ACCESSION NUMBER: humangp/chr19-q96g16
DATABASE ENTRY DATE: 2003-04-22
US-10-878-556A-158
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTAWA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
Sequence 975, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
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Best Local Similarity 26.0*
Marches 20; Conservative
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ORGANISM: Homo sapiens
US-10-821-234-975
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JAPPLICANT: Trepod, Catherine

APPLICANT: Trepod, Catherine

APPLICANT: Trepod, Catherine

APPLICANT: Trepod, Catherine

TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND ME

TITLE OF INVENTION: USE

TITLE OF INVENTION: USE

TITLE OF INVENTION: USE

CURRENT APPLICATION NUMBER: US/11/194,246

CURRENT FILING DATE: 2005-08-01

PRIOR PRIOR PRILING DATE: 2002-10-21

PRIOR PRILING DATE: 2001-10-19

NUMBER: OF SEQ ID NOS: 621

SOFTWARE: PatentIn version 3.0

SEQ ID NO 316

LENGTH: 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 VKEVTKLIDNNKTEKEILDAFDKMCSKLPKSL---SEECQ------EVVD------ 52
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                                                                                                                                                                                                                                                                                                                                                                                                     24; Indels 21;
                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 14.8%; Score 61; DB 7; Length 292; 1 Similarity 29.0%; Pred. No. 9; 20; Conservative 9; Mismatches 20; Indels
TITLE OF INVESTIGATION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 5296
LENGTH: 115
                                                                                                                                                                                                                                                                                                                                                    Score 61.5; DI
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                    Query Match 14.9%; Score 61.5; D
Best Local Similarity 20.5%; Pred. No. 2.6;
Matches 17; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 SKSFASSLLPLSVTNFTTDMACT 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 --TYGSSILSILLERVSPELVCS 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: HAEMOPHILUS INFLUENZAE
                                                                                                                                                                                                                                                                              ) ORGANISM: Neisseria gonorrhoeae US-10-467-657-5296
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Best Local Similarity
Matches 20; Conserva
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SEQ ID NO 281
LENGTH: 2036
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| Sequence 280. Application US/11124368A
| Publication No. US20050287559A1
| GENERAL INFORMATION:
| APPLICANT: Michael Cargill
| APPLICANT: May Luke
| TITLE OF INVENTION: Genetic Polymorphisms Associated with
| TITLE OF INVENTION: Usecular Diseases, Methods of Detection and Uses Thereof
| TITLE OF INVENTION: Usecular Diseases, Methods of Detection and Uses THIR REFERENCE: CLO01524
| CURRENT APPLICATION NUMBER: US 60/568,845
| PRIOR FILING DATE: 2004-05-07
| PRIOR PLICATION NUMBER: US 60/625,936
| PRIOR PLILOG DATE: 2004-11-09
| WUMBER OF SEQ ID NOS: 21112
| SEQ ID NO 280
| LENGTH: 2036
| LENGTH: 2036
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REPERINCE: CL001524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT APPLICATION NUMBER: US 60/568,845
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR PILING DATE: 2004-05-07
PRIOR PILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 276
LENGTH: 2036
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14.6%; Score 60; DB 7; Length 2036;
Best Local Similarity 25.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 16; Mismatches 25; Indels
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Best Local Similarity 25.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 16; Mismatches 25;
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CORGANISM: Homo sapiens
US-11-124-368A-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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US-11-124-368A-280
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APPLICANT: Michele Cargill
APPLICANT: Manes J. Devlin
APPLICANT: Manes J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CLO01524
CURRENT APPLICATION NUMBER: US 60/568,845
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR APPLICATION NUMBER: US 60/568,945
RRIOR APPLICATION NUMBER: US 60/568,945
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; Sequence 916, Application US2005025114A1
; Publication No. US2005025114A1
; GENERAL INFORMATION:
    APPLICANT: Labat, Ivan
    APPLICANT: Stache-Crain, Birgit
    APPLICANT: Andarmani, Susan
    APPLICANT: Andarmani
    APPLICANT: Andarmani
    APPLICANT: Andarmani
    APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 KLIDNNKTEKEILDAFDKMCS-KLPKSLSEE-------COEVVDTYGSSILSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CEFL------VKEVTKLIDNNKTEKEI-LDAFDKMCSKLPKSLSEECQE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3002;
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14.4%; Score 59.5; DB 6;
Best Local Similarity 27.8%; Pred. No. 2.2e+02;
Matches 25; Conservative 8; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.6%; Score 60; DB 7; Best Local Similarity 25.3%; Pred. No. 1.2e+02; Matches 20; Conservative 16; Mismatches 25
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US-09-940-308-3
; Sequence 3, Application US/09940308
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US-11-124-368A-281
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; ORGANISM: Homo sapiens
US-10-821-234-916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VCBFLVKBVTKLIDNNKT--EKBILDAPDKMC--SKLPKSLSEEC--QEVVDTYGSS 57
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APPLICANT MINISTER.

TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as TITLE OF INVENTION: an Immunosuppressive Agent TITLE OF INVENTION: US/09/940,308

CURRENT PILING DATE: 2001-08-27

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1995-11-05

PRIOR FILING DATE: 1995-11-04

NUMBER OF SEQ ID NOS: 16

SOCTHWARE: RESULT 1995-01-24

NUMBER OF SEQ ID NOS: 16

SEQ ID NOS: 
                                                                            GENERAL INFORMATION:
APPLICANT: Murgita, Robert A.
TITLE OF INVENTION: An Immunosuppressive Agent
CURRENT APPLICATION NUMBER: US/09/940,308
CURRENT FILING DATE: 2001-08-27
RICA APPLICATION NUMBER: US 09/186,723
PRIOR PILING DATE: 1998-11-05
PRIOR PILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FREEEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.3%; Score 59; DB 5; Length 197;
Best Local Similarity 35.1%; Pred. No. 9.3;
Matches 20; Conservative 10; Mismatches 21; Indels
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14.3%; Score 59; DB 5; Length 389;
Best Local Similarity 35.1%; Pred. No. 21;
Matches 20; Conservative 10; Mismatches 21; Indels
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Publication No. US20040092437A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapiens
US-09-940-308-3
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ORGANISM: Homo sapiens
US-09-940-308-6
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Search completed: January 13, 2006, 16:39:05 Job time : 1.5894 secs

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Query Match 100.0%; Score 412; DB 1; Length 80; Best Local Similarity 100.0%; Pred. No. 6.9e-42; Matches 80; Conservative 0; Mismatches 0; Indels
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US-08-100-247-3
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Sequence 6272, Ap
Sequence 23, Appl
Sequence 8603, Ap
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                                                                                                    January 13, 2006, 16:26:00; Search time 8.34437 Seconds (without alignments) 792.637 Million cell updates/sec
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Sequence 3,
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Sequence 2,
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Sequence 3,
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412
1 SDVYCEVCEFLVKEVTKLID......ILLBEVSPELVCSMLHLCSG
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2: /cgn2 6/ptodata/1/laa/6_COMB.pep:*
3: /cgn2 6/ptodata/1/laa/H_COMB.pep:*
4: /cgn2 6/ptodata/1/laa/PCTUS_COMB.pep:*
5: /cgn2 6/ptodata/1/laa/RR_COMB.pep:*
6: /cgn2 6/ptodata/1/laa/RR_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-08-483-146A-3

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US-08-722-513A-4

US-08-756-031-3

US-08-928-074-24

US-08-100-247-2

US-08-100-247-2

US-08-484-594A-2

US-08-484-594A-2

US-08-780-748-1

US-08-949-016-6272

US-09-949-016-6272

US-09-148-594A-1

US-08-231-159-1

US-08-231-159-1

US-08-231-159-1

US-08-11-159-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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US-08-756-031-1 US-08-928-074-1 US-09-231-159-8	US-08-611-307-8 US-08-928-074-8 US-09-780-438C-3 US-09-780-438C-5	US-09-780-438C-6 US-09-780-438C-4 US-08-483-146A-9 US-08-232-513A-18	US-08-484-594A-9 US-09-231-159-7 US-08-611-307-7	US-09-076-258A-9 US-08-928-074-7 US-10-339-351-2 US-08-596-684F-6
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## ALIGNMENTS

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Sequence 3, Application US/08100247

Patent No. 5571787

GENERAL INFORMATION:

APPLICANT: O'BRIEN, JOHN S.

APPLICANT: C'RINCON, YASUO

TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR

STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR

CITY: NEWPORT BRACH

STATE: CAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
COUNTRY: USA
ZIP: 92660

ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SISTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,247
FILING DATE: 19930730
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
MARKE: ISRAELSER: 19930730
CLASSIFICATION NUMBER: 29,655
REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: 09,655
TELECOMMUNICATION HYRORMATION:
THE HYRORMATION:
TELECOMMUNICATION HYRORMATION:
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USA
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                                                                                                                                                                                                                                                                         APPLICANT: O'BLIEN, John S.
APPLICANT: Kishimoto, Yasuo
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
TITLE OF INVENTION: THEREFROM
NUMBER OF SEQUENCES: 11
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Blvd. 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
9
                    SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS 60
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1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASSESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,146A
FILING DATE: O'-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 24
RETING DATE:
RILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: 18 REABENC.
TELEBHONE: 619-235-955
TELEBHONE: 619-235-956
                                                                                                                                                                                                                Sequence 3, Application US/08483146A Patent No. 5696080 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ILLEEVSPELVCSMLHLCSG 80
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                                                                                                        61 ILLEEVSPELVCSMLHLCSG 80
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SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein PRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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Matches 80; Conserva
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STRANDEDNESS: 813
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                                                                                                                                                                                 RESULT 2
US-08-483-146A-3
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; Sequence 4, Application US/08232513A

US-08-232-513A-4

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1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS
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US-08-484-594A-3
IS-08-484-594A-3
| Sequence 3, Application US/08484594A
| GENERAL INFORMATION:
| APPLICANT: Kishimoto, Yasuo
| TITLE OF INVENTION: USB OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
| TITLE OF INVENTION: DERIVED THEREFROM
| NUMBER OF SEQUENCES: 11
| CORRESPONDENCES: 11
| CORRESPOND
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GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
TILLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
TILLE OF INVENTION: as Therapeutic Agents
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 412; DB 1; Length 80; 100.0%; Pred. No. 6.9e-42; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER KEADABLE FORM:
MEDIUW TYEE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,513A
FILING DATE: 21-APR-1994
CLASSITCATION NUMBER: US/08/100,247
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-UD 1643
TELECOMMUNICATION INFORMATION:
TELEBEHONE: (619) 535-9001
TELEBEHONE: (619) 535-9001
TELERENT. (619) 535-9049
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERLETICS:
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OTHER INFORMATION: /label= Saposin_C
US-08-232-513A-4
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Best Local Similarity 100.0
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 80 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS 60
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; Sequence 3, Application US/08756031
; Patent No. 6590074
; GENERAL INFORMATION:
    APPLICANT: O'BRIEN, JOHN S.
    APPLICANT: KISHIMOTO, YASUO
    TITLE OF INVERTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR NUMBER OF SEQUENCES: 5
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
    STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
    CITY: NEWPORT BEACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 412; DB 2; Length 80; Best Local Similarity 100.0%; Pred. No. 6.9e-42; Matches 80; Conservative 0; Mismatches 0; Indels
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ZIP: 92660
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,031
FILING DATE: 26-NOV-1996
CLASSIFICATION NUMBER: 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REFERENCE/DOCKET NUMBER: 29,655
REFE
PRICE DATE: 28-OCT-97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/483,146
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: 1sraelsen, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: MYBLOS.2DV1C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION I
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SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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Fatent No. 6559124

GENERAL INFORMATION:
APPLICANT: Kishimoto, Yasuo
TITLE OF INVENTION: FHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: THEREFROM
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 11
CORRESPONDENCE ADDRESS: 11
CORRESPONDENCE ADDRESS: 1
COUNTRY: Usewort Center Blvd. 16th Ploor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
COUNTRY: USA
TIPLE OF INVENTION: Windows Version 2.0
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/076,258A
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                                                                                                                                                                          COMPUTER: 18M COMPACTALE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,594A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISFASION NUMBER: 29,655
REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: WIELOS:002DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958.970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ILLEEVSPELVCSMLHLCSG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 80; Conservative 0
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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1 SDVYCEVCEFLVKEVTKLIDNNKTEKBILDAFDKMCSKLPKSLSBECOBVVDTYGSSILS
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ANTI-SENSE: NO
FRAGMENT TYPE: N-termi
IMMEDIATE SOURCE:
-ANK: PROSAPOSIN
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US-08-483-146A-2
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Sequence 24, Application US/08928074
Sequence 24, Application US/08928074
GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STREET: CA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 412; DB 2; Length 80; 100.0%; Pred. No. 6.9e-42; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             Query Match 100.0%; Score 412; DB 2; Length 80; Best Local Similarity 100.0%; Pred. No. 6.9e-42; Matches 80; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: CA
COUNTRY: CA
COUNTRY: GA
ZIP: 92037
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,074
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/611,307
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/04143
FILING APPLICATION NUMBER: PCT/US97/04143
FILING DATE: 05-MAR-1996
ATTORNEY/ACET INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38.347
REGISTRATION NUMBER: 38.347
REGISTRATION NUMBER: 07256/024001
TELECOMMUNICATION INFORMATION:
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ILLEEVSPELVCSMLHLCSG 80
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Best Local Similarity 100.
Matches 80; Conservative
                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-928-074-24
                                                                                                                                                               internal
                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE: inter
IMMEDIATE SOURCE:
CLONE: SAPOSIN C
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310 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKWCSKLPKSLSEECQEVVDTVGSSILS 369
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1 SDVYCEVCEFLVKEVTKIJNNKTEKEILDARDKMCSKLPKSLSEECQEVVDTYGSSILS
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; Sequence 2, Application US/08100247
; Patent No. 5571787
; GENERAL INFORMATION:
    APPLICANT: O'BRIBN, JOHN S.
    APPLICANT: KISHIMOTO, YASUO
; TITLE OF INTENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
    ADDRESSEE: KNOBER, MARTENS, OLSON AND BEAR
    STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITY: NEWPORT BEACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 523;
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100.0%; Score 412; DB 1; Length 5
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0; Indels
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ZIP: 92660
COMPUTER SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Pl
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LENGTH: 523 amino acids
TYPB: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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310 SDVYCEVCEPLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS 60
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1 Sequence 2, Application US/08484594A

2 Sequence 2, Application US/08484594A

3 Patent No. 5714459

GENERAL INFORMATION:

APPLICANT: O' Barien, John S.

APPLICANT: Kishimoto, Yasuo

TITLE OF INVENTION: DERIVED THEREFROM

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEB: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Drive, Sixteenth Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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  COMPUTER ASSESSED

MEDIUM TYPE: Ploppy disk
COMPOTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,513A
FILING DATE: 21-APR-1994
CLASSIFICATION NUMBER: US 08/100,247
PLING DATE: 30-JUL-1993
ATYORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-UD 1643
TELECOMMUNICATION INFORMATION:
TELEFRAK: (619) 535-9001
TELEFRAK: (619) 535-9001
TELEFRAK: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRACTERISTICS:
'PWATH. 523 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTED FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,594A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/100,247
FILING DATE: 30-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: Protein
; LOCATION: 1..523
; OTHER INFORMATION: /label= Hum_prosaposin
US-08-232-513A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 ILLEEVSPELVCSMLHLCSG 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 523 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92660
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                  APPLICANT: O'BRIEN, John S.
APPLICANT: Kishimoto, Yasuo
APPLICANT: Kishimoto, Yasuo
APPLICANT: Kishimoto, Yasuo
TITLE OF INVENTION: COMPRISING PROSAPOSITIONS
TITLE OF INVENTION: THEREFROM
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Blvd. 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 SDVYCEVCEPLVKEVTKLIDNNKTEKEILDAPDKWCSKLPKSLSEECQEVUDTYGSSILS 369
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Patent No. 5700909

GENERAL INFORMATION:

APPLICANT: O'Brien, John S.

TITLE OF INVENTION: Brosaposin and Cytokine-Derived Peptides

TITLE OF INVENTION: As Therapeutic Agents

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San.Dlego

STATE: California

COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: OSYTEM: DOS
SOPTWARE: PSETENC FOR Windows Version 2.0
CURSENT APPLICATION DATA:
RILING DATE: 07-JUN-1995
CLASSIPICATION DATA:
PRICA APPLICATION DATA:
APPLICATION NUMBER:
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100.0%; Score 412; DB 1.
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY JAGENT INFORMATION:
NAME: laraleen, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: MYELOS.002DV1
TELECOMMUNICATION INFORMATION:
TELECPHONE: 619-235-850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 523 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-483-146A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-232-513A-3
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STATE: CA
COUNTRY: US
ZIP: 92660
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US-08-756-031-2
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GENERAL INFORMATION:

APPLICANT: O'Brien, John S.

APPLICANT: O'Brien, John S.

APPLICANT: O'Brien, John S.

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: THEREFROM

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Blvd. 16th Floor

CITY: Newport Beach

STREET: Correspondence Address S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 412; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,258A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIPCATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/958.970
FILING DATE: 28-0CT-97
PRIOR APPLICATION NUMBER: 08/483,146
FILING DATE: 07-UN-1995
APPLICATION NUMBER: 08/100,247
FILING DATE: 30-UL-1993
ATTORNEY AGENT INFORMATION:
NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29,655
REFERBNICE/DOCKET NUMBER: 29,655
THEREOMENINE/CATION INFORMATION:
THEREOMENINE/CATION INFORMATION:
THEREOMENINE/CATION INFORMATION:
                                                                                                                        MYELOS.002DV2
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Patent No. 6559124
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                             REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: 29,655
REPRENCE/POCKET NUMBER: MYELGENCOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal US-08-484-594A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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310 SDVYCEVCEFLVKEVTKLIDNNKTEKBILDAPDKWCSKLPKSLSEBCQEVVDTYGSSILS 369
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; Patent No. 659074
; GENERAL INFORMATION:
APPLICANT: O'BRIEN, JOHN S.
APPLICANT: KISHIMOTO, YASUO
TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: KNOBER, MATTENS, OLSON AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITTLE OF THE OF THE OFFER OFFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC compactible
COMPUTER: Elem PC compactible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,031
FILING DATE: 26-NOV-1996
CLASSTRICATION: 514
PRIOR DATE: 30-NUL-1993
APPLICATION NUMBER: 08/100,247
PILING DATE: 30-NUL-1993
APPLICATION NUMBER: 08/100,247
RELIGHERON INFORMATION:
NAME: BEABLEAT NUMBER: 29,655
REFRENCE/DOCKET NUMBER: 29,655
REFRENCE/DOCKET NUMBER: 0BRIEN.002A
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 412; DB 2;
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 ILLEEVSPELVCSMLHLCSG 389
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ILLEEVSPELVCSMLHLCSG
                                                                                                    EENGTH: 523 amino acids
TYPE: amino acid
STRANDENNESS: single
MOPLOGY: linear
MORGULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-09-076-258A-2
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-term immediate Source: CLONE: PROSAPOSIN US-08-756-031-2
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LENGTH: 524
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| Sequence 6272, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION; POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION; POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| CURRENT APPLICATION NUMBER: 00/2914, 155
| PRIOR APPLICATION NUMBER: 60/241, 755
| PRIOR PILING DATE: 2000-10-03
| PRIOR APPLICATION NUMBER: 60/231, 498
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NO 6272
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09352548
| Sequence 1, Application US/09352548
| Patent No. 6500431
| GENERAL INFORMATION:
| APPLICANT: Gill, Parkash S. |
| TILE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth FILE REFRENCE: 017986-000410US |
| TILE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth FILE REFRENCE: 017986-000410US |
| CURRENT FILING DATE: 1999-07-12 |
| EARLIER PRILING DATE: 1999-07-13 |
| EARLIER PILING DATE: 1998-07-13 |
| SEQITWARE: PatentIn Ver. 2.1 |
| SEQITURE FILE SEQIENCE: 0170-0713 |
| TYPE: PRT |
| TYPE: PRT |
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                                                                                                                                    310 SDVYCEVCEPLVKEVTKLIDNNKTEKEILDAFDKWCSKLPKSLSEECQEVVDTYGSSILS 369
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Query Match
100.0%; Score 412; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 412; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 8e-41;
Matches 80; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                            61 ILLEEVSPELVCSMIHLCSG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: PEPTIDE
LOCATION: (195)...(275)
COTHER INFORMATION: Saposin B
US-09-352-548-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-949-016-6272
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                                                                                                  Query Match 100.0%; Score 412; DB 2; Length 524; Best Local Similarity 100.0%; Pred. No. 8e-41; Matches 80; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                    371 illeevspelvcsmihlcsg 390
                                                                                                                                                                                                                                                                                                                      61 ILLEEVSPELVCSMLHLCSG 80
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6272
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GenCore version 5.1.6
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OM protein - protein search, using sw model

January 13, 2006, 16:23:49

; Search time 6.35762 Seconds (without alignments) 1210.728 Million cell updates/sec

US-10-801-517-2 412 1 SDVYCEVCEPLVKEVTKLID.....ILLEEVSPELVCSMLHLCSG Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR 80:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		×				
Result No.	Score	Query Match	Query Match Length	08	ΙD	Description
-	412	100.0	527	-	SAHUP	saposin precursor
8	343	83.3	80	~	S21770	saposin-C - bovine
e	261	63.3	81	7	A32026	glucosylceramide b
4	193		554	٦	A28716	saposin precursor
'n	168	40.8	557	ч	JH0604	saposin precursor
ø	158	38.3	965	~	T00207	P109 protein - sil
7	106.5	25.8	217	~	T48201	
8	106	25.7		~	T46069	hypothetical prote
6	106	25.7	428	~	S47096	
10	106	25.7	474	~	T12049	
11	104	25.2	206	N	F86253	hypothetical prote
12	103	25.0	292	~	T14446	aspartic proteinas
13	103	25.0	322	7	S41400	aspartic proteinas
14	103	25.0	433	~	E96649	hypothetical prote
15	102.5	24.9	376	~	S02766	pulmonary surfacta
16	102	24.8	206	~	T07915	probable aspartic
17	102	24.8	509	~	JC7272	
18	100	24.3	513	~	T11686	aspartic proteinas
19	99.5	24.2	103	~	D89567	protein T08A9.8 [i
20	99.5	24.2	363	~	A29072	pulmonary surfacta
21	66	24.0		н	A40292	
22	98	23.8	496	N	JS0732	aspartic proteinas
23	97	23.5	508	~	S19697	
24	97	23.5	509	~	866516	
25	97	23.5	513	~	T09739	aspartic endopepti
26	96.5	23.4	101	н	849145	amoebapore C precu
27	95	23.1		-	LNPG1	pulmonary surfacta
28	95	23.1	369	N	146531	surfactant protein
29	92	22.3	509	~	S49349	cyprosin (EC 3.4.2

pulmonary surfacta pulmonary surfacta	probable aspartic	amoebapore B precu	amoebapore A precu	protein T08A9.7 [i	hypothetical prote	hypothetical prote	NK-lysin protein -	aspartic proteinas	protein T08A9.9 [i	endostyle-specific	protein T08A9.10 [	aspartic proteinas	sphingomyelin phos	hypothetical prote
LNRBB	D85056	849144	825283	B89567	T15674	T15676	S55044	PC4080	E89567	T00617	C89567	S71591	T27869	T09915
	(1)	н	Н	~	~	~	~	7	~	~	~	~	7	7
370	208	96	98	202	314	195	129	280	223	650	74	206	572	306
22.1	22.1	22.0	22.0	21.7	21.6	21.1	20.5	20.0	19.8	19.2	19.1	18.9	18.8	18.4
91	16	90.5	90.5	89.5	89	87	84.5	82.5	81.5	79	78.5	78	77.5	16
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

7	
3505	HILL

Alternate names: cerebroaide sulfate activator protein; co-beta-glucosidase; componen mia (SAP); sphingolipid activator protein A2; sulfatide sulfatase activator protein N;Alternate names: cerebroaide sulfate activator protein N; contains: prosaposin; saposin A; saposin B; saposin D C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Jun-1992 #sequence revision 17-Nov-1995 #text change 09-Jul-2004 C;Date: 30-Jun-1992 #sequence revision 17-Nov-1995 #text change 09-Jul-2004 C;Date: 30-Jun-1992 #sequence revision 17-Nov-1995 #text change 09-Jul-2004 C;Date: 30-Jun-1902 #sould N; Silva N; N;Nakano, T.; Sandhoff, K.; Stuemper, J.; Christomanou, H.; Suzuki, K.
J. Blochem. 105, 152-154, 1989 A;Jul-length cDNA coding for sulfatide activator, a Co-beta-glucos A;Reference number: JX0061; MuID:89255151; PMID:2498298

A;Molecule type: mRNA A;Residues: 1-527 <NMK: A;Cross-references: UNIPROT:P07602; UNIPARC:UP1000002B33D; GB:D00422; NID:G220063; PIDN A;Note: alternative splice form 1

A; Accession: A57368

A; Molecule type: mRNA
A; Residues: 1-259, 263-527 < NA2>
A; Residues: 1-259, 263-527 < NA2>
A; Residues: 1-259, 263-527 < NA2>
A; Crose-references: UNIPARC: UP10000000BP; GB:J03015; GB:J03086; NID:g337755; PIDN:AAB5
A; Note: alternative splice form 2
B; Rorman, E.G.; Scheinker, V.; Grabowski, G.A.
Genomics 13, 312-318, 1992
A; Title: Structure and evolution of the human prosaposin chromosomal gene.
A; Reference number: A42003; MUID:92307663; PMID:1612590
A; Accession: A42003

A;Molecule type: DNA
A;Residues: 50-140 <ROR>
A;Cross-references: UNIPARC;UPI00001741AA; GB:M86181
A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107236)
A;Accession: B42003

A;Accession: C42003
A;Rolecule type: DNA
A;Residues: 305-393 <R03>
A;Residues: 305-393 <R03>
A;Cross-references: UNIPARC:UPI00001741AD
A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107238); sequence in A;Accession: D42003 A;Molecule type: DNA A;Residues: 185-259;263-276 <RO2> A;Cross-references: UNIPARC:UPI00001741AB; UNIPARC:UPI00001741AC A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107237)

A; Molecule type: DNA A; Residues: 399-487 <RO4> A; Cross-recences: UNIPARC: UPI00001741AE A; Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107239); sequence ir R; Rorman, E.G.; Grabowski, G.A. Reconnatos 5, 486-492, 1989 A; Title: Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sphi A; Reference number: A30367; MUID:90129043; PMID:2515150

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A; Cross-references: UNIPARC: UPI000000DBF; GB: M32221; NID: 9337761; PIDN: AAA60303.1; PID:
                                A; experimental source: lymphoblast A; Accession: C35985
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   Alacession: A1035,
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A, Accession: B35985
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Residues: 1-259, 263-527 < KR2>
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Residues: 213-221 <KRE>
Cross-references: UNIPARC:UP100001741B6; GB:M32221
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A; Modecule type: mRNA
A; Residues: 213-216, 17, 218-221 < KR3>
A; Residues: 213-216, 17, 218-221 < KR3>
A; Cross-references: UNIPARC:UP100001741B7
A; Note: sequence from patients with activator-deficient metachromatic leukodystrophy; th
R; Fuerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.B.; Sandhoff, K.
R; Fuerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.B.; Sandhoff, K.
A; Fuerst, Te.; The complete amino-acid sequences of human ganglioside GM2 activator protein an
A; Reference number: S13195; MUID:91006165; PMID:2209618
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A;Molecule type: protein
A;Residues: 195-259,263-276 <KLE>
A;Residues: 195-259,263-276 <KLE>
A;Cross-references: University W.; Sandhoff, K.
B;Puerst, W.; Machleidt, W.; Sandhoff, K.
Biol. Chem. Hoppe-Seyler 369, 317-328, 1988
A;Fitle: The precursor of sulfatide activator protein is processed to three different payseference number: S00813; MUID:89000190; PMID:3048308
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Biol. Chem. Hoppe-Seyler 368, 1571-1578, 1987
A;Title: Complete amino-acid sequence and carbohydrate content of the naturally occurris
A;Reference number: S00226; MUID:88163077; PMID:3442600
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A, Residues: 314-393 «KL2.
A, Residues: 314-393 «KL2.
A, Croser-references: UNIPARC: UPI000003ED8E
A, Croser-references: UNIPARC: UPI000003ED8E
A, Croser-references: UNIPARC: UPI000003ED8E
A, Fither: 270, 9953-9960, 1995
A, Fither: Structural analysis of saposin C and B. Complete localization of disulfide brid A, Reference number: A57297; MUID: 95247790; PMID: 7730378
A, Contents: annotation, disulfide bonds; glycosylation
A, Reference number: A57297; MUID: 95247790; MID: 9708971410n
A, Contents: annotation, disulfide bonds; glycosylation
A, Contents: annotation, disulfide bonds; glycosylation
A, Contents: A, Sandhoff, K.; Fuerst, W.; Kwon, H.Y.; Schnabel, D.; Suzuki, K.
FEBS Lett. 280, 267-270, 1991
A, Title: The organization of the gene for the human cerebroside sulfate activator prote:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 60-84; 86-107, 109-119, 125-134 < MOR>
A; Residues: 60-84; 86-107, 109-119, 125-134 < MOR>
A; Residues: 60-84; 86-107, 109-119, 109-1199; MIPARC: UPI00001741BB; B; Conserved and Conserved
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A; Residues: 'GSSR', 18-259, 263-299, 'D', 301-302, 'D', 304-527 <OAB>
A; Cross-references: Unitarity (GB:003086
B; Dewji, N.N.; Wenger, D.A.; O'Brien, J.S.
Proc. Natl. Acad. Sci. U.S.A. 84, 8652-8656, 1987
A; Title: Nucleotide sequence of cloned cDNA for human sphingolipid activator protein 1 kA; Reference number: S02289; MUID:88068647; PMID:285502
A; Stetus: significant semicer.
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A; Residues: 195-259, 263-277 < FUE>
A; Cross-references: UNIPARC: UPI00001741B8
R; Morimoto, S.; Martin, B.M.; Yamamoto, Y.; Kretz, K.A.; O'Brien, J.S.; Kishimoto, Proc. Natl. Acad. Sci. US.A. 86, 31389-3393, 1989
A; Title: Saposin A: second cerebrosidase activator protein.
A; Reference number: A32784; MUID: 89240739; PMID: 2717620
A; Accession: A32784
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A; Molecule type: mRNA
A; A; Molecule type: mRNA
A; A; Mote: this sequence corrected by A41240
A; Note: this sequence corrected by A41240
A; Note: part of this sequence, including the amino end o A; Note: part of this sequence, including the amino end o A; Note: part of this sequence, including the amino end o A; Note: part of this sequence, 1361-1365, 1988
A; Mille: Complete amino-acid sequence of the naturally o A; Reference number: S02028; MUID: 89207118; PMID: 3242555
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A;Residues: 410-487 <FU2>
A;Cross-references: UNIPARC:UP100001741BF
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saponin precursor - rat
Nathernate names: cerebroside sulfate activator protein; co-beta-glucosidase; componential (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfat
N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A28716
B;Collard, M.W.; Sylvester, S.R.; Tsuruta, J.K.; Griswold, M.D.
B;Cohemistry 27, 4557-4564, 1988
A;Title: Blosynthesis and molecular cloning of sulfated glycoprotein 1 secreted by rat
A;Reference number: A28716; MUD:89000647; PMID:3048385
A;Accession: A28716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-554 <COL>
A;Cross-references: UNIPROT: P10960; UNIPARC: UP1000013555D; GB:M19936; NID:g206904; PIDN
A;Note: parts of this sequence, including the amino end of the mature protein, were det
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function:

C; Function:

A; Description:

A; Description:

A; Description:

A; Description:

A; Note: saposins A and C (SAP-2) activate hydrolysis of glucocerebroside by beta-glucos*

A; Note: saposins B (SAP-1) activates hydrolysis of glactocerebroside by beta-glucos*

A; Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside by arylsul

A; Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiester

C; Superfamily: saposin repeat homology

C; Superfamily: saposin repeat homology (SAP-)

F; 1-16/Domain: signal sequence #status predicted <SIG>
F; 1-554/Product: prosaposin #status predicted <SIG>
F; 1-554/Product: saposin Repeat homology (SAP-)

F; 189-280/Domain: saposin A #status predicted (SAP-)

F; 189-280/Domain: saposin Repeat homology (SAP-)

F; 190-397/Domain: saposin repeat homology (SAP-)

F; 191-389/Product: saposin Predicted (SAP-)

F; 191-389/Product: saposin Repeat homology (SAP-)
3 VTCKACEYVVKKVMELIDNNRTEEKIIHALDSVCALLPESVSEVCQEVVDTYGDSIVALL
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372 MHEVNPNFLCGVISLCS 388
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63 LOEMSPELVCSELGLC 78
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                                                                             63 LEBVSPELVCSMLHLC
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R;Sance, A.; Mizuno, T.; Kondoh, K.; Hineno, T.; Ueno, S.; Kakimoto, Y.; Morita, N.
Biochim. Blophys. Acta 1120, 75-80, 1992
A;Title: Saposinc from bovine spleen; complete amino acid sequence and relation between A;Reference number: $21770; MUID:92207994; PMID:1554743
                                                                             A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 59-125 <RBS>
A,Cross-references: UNIPARC:UPI000016A751; EMBL:X57107; NID:930234; PIDN:CAA40391.1; PID
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R;Sano, A.; Radin, N.S.; Johnson, L.L.; Tarr, G.E.
J. Biol. Chem. 265, 19597-19601, 1988
A;Title: The activator protein for glucosylceramide beta-glucosidase from guinea pig liv
A;Reference number: A32026; MUID:89066787; PMID:3198642
A;Accession: A32026
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C,Species: Cavia porcellus (guinea pig)
C,Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Bos primigenius taurus (cattle)
Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDVYCEVCEFLVKEVTKIJDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILS
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                                                                                                                                                                                                                                                                     DB 1; Length 527;
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                                                                                                                                                                                                                                                                                                                                               Indels
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A;Residues: UNIPARC:UP1000013555A
A;Crose.references: UNIPROT:P20097; UNIPARC:UP1000013555A
C;Superfamily: saposin; saposin repeat homology
R;1-81/Domain: saposin repeat homology <SAP>
       A; Reference number: 137264; MUID: 91192146; PMID: 2013321
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Best Local Similarity 100.0%; Pred. No. 5e-32;
Matches 80; Conservative 0; Mismatches (
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C; Superfamily: saposin; saposin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 ILLEEVSPELVCSMLHLCSG 393
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                                              A; Accession: 137265
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NyAlternate names: cerebroside sulfate activator protein; co-beta-glucosidase; componentin (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfat NiContains: prosaposin; saposin A; saposin B; saposin C; saposin D C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: JH0604
E; Tabada, M.; Sakiyama, T.; Endo, H.; Kitagawa, T.
Biochem. Biophys Res. Commun. 184, 1266-1272, 1992
A; Title: The primary structure of mouse saposin.
A; Reference number: JH0604; MUID: 92272718; PMID: 1590788
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                                                                                                                                                                                        312 IFCQVCQLWMRKLSELLINNATEELLIKGLSKACSLLPAPASTKCQEVLVTFGPSLLDVL 371
                                                                                                                                                 3 VYCEVCEPLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECOEVVDTYGSSILSIL 62
                                                                          Gaps
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DB 1; Length 554;
46.8%; Score 193; DB 1; Length 55
40.3%; Pred. No. 6.1e-11;
ive 24; Mismatches 22; Indels
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20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
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A;Note: T18N14.110
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185 FLEKKDVCTILHVCPG 200
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A;Introns: 30/1; 7
A;Note: T20L15.70
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Matches 2
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         A; Molecule type: mRNA
A; Cross -references: UNIPROT: 061207; UNIPARC: UPI0000170C25; GB: S36200; NID: 9249386; PIDN:
A; Experimental source: liver
C; FRUCTION: saposins bind sphingolipids, form hydrophilic complexes and make them acc
A; Pathway: sphingolipid catabolism
A; Note: saposins A and C (SAP-2) activates hydrolysis of galactocerebroside by beta-glucosy
A; Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside by beta-glucosy
A; Note: saposin B (SAP-1) activates hydrolysis of sphingomyelin by sphingomyelin phosphodiestera
C; Superfamily: saposin; saposin repeat homology
C; Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome; sph
C; Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome; sph
C; Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome; sph
C; Feys-148/Domain: saposin Retatus predicted <SAPO>
F; 194-276/Froduct: saposin Repeat homology <SAPO>
F; 194-276/Froduct: saposin D #status predicted <SAPO>
F; 194-276/Froduct: saposin D #status predicted <SAPO>
F; 194-217/Froduct: saposin D #status predicted <SAPO>
F; 194-217, Product: saposin D #status predicted <SAPO>
F; 194-2131, 194-217, 200-267, 229-240, 317-390, 317-390, 48, 314, 314, 314, 319, 419-515, 445-509, 4
F; 100, 214, 334, 379, 459/Binding site: carbohydrate (Asn) (covalent) #status predicted
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CiAccession: T00207
RiTamburni, J.; Chang, P.K.; Li, H.; Natori, M.
Gene 212, 287-293, 1998
A;Title: Molecular cloning of a cDNA encoding a silkworm protein which contains the cons A;Reference number: 214124; MUID:98278844; PMID:9611271
A;Accession: T00207
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-965 cTAM>
A;Residues: 1-965 cTAM>
A;Crosss-references: UNIPROT:015997; UNIPARC:UPI00007B54A; EMBL:AB008449; NID:g2575864; F;778-870/Domain: saposin repeat homology <SAP3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILSIL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .Species: Bombyx mori (silkworm)
.Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
.Accession: T00207
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40.8%; Score 168; DB 1;
Best Local Similarity 36.4%; Pred. No. 1.6e-08;
Matches 28; Conservative 20; Mismatches 29.
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Matches
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C;Accession: T48201
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mewsumitted to the Protein Sequence Database, March 2000
A;Reference number: 224488
A;Accession: T48201
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9LZW6; UNIPARC:UPI00000A6022; EMBL:AL162351
A;Experimental source: cultivar Columbia; BAC clone T20115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cynarase (EC 3.4.23.-) - cardoon
C;Species: Cynara cardunculus (cardoon)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Aug-1997
C;Accession: S47096
R;Cordeiro, M.C.; Xue, Z.T.; Pietrzak, M.; Pais, M.S.; Brodelius, P.
submitted to the EMBL Data Library, November 1992
A;Description: Tissue specific expression of cynarase (s) genes in flowers of Cynara ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypochetical protein T18N14.110 - Arabidopsis thaliana ($Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46069
R;Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.; submitted to the Protein Sequence Database, December 1999
A;Reference number: 223013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ?
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A;Molecule type: DNA
A;Residues: 1-213 <-OBL-3
A;Cross-references: UNIPROT:Q9SCT5; UNIPARC:UPI00000AC273; EMBL:AL132968
A;Experimental source: cultivar Columbia; BAC clone T18N14
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25.7%; Score 106; DB 2; Length 213;
Best Local Similarity 29.7%; Pred. No. 0.0052;
Matches 22; Conservative 16; Mismatches 34; Indels
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Gaps

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C;Superfamily: oryzasin; saposin repeat homology

A;Status: preliminary

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A;Molecule type: mRNA
A;Residues: 1-292 <FUJ>
A;Cross-references: UNIPROT:Q43407; UNIPARC:UPI00000AC977; EMBL:X77260; NID:g459425; PI
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A; Cross-references: UNIPROT:043407; UNIPARC:UP10000175D78; EMBL:X77260
A; Cross-references: UNIPROT:043407; UNIPARC:UP10000175D78; EMBL:X77260
C; Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent (C; Superfamily: oryzasin; saposin repeat homology
C; Keywords: aspartic proteinase; hydrolase
E; 99:144/Domain: asposin repeat homology #status atypical <SAP1>
F; 153-203/Domain: asposin repeat homology #status atypical <SAP2>
F; 73/Active site: Asp #status predicted
                                                                                                                                                                                                                                                                                                                                            aspartic proteinase (BC 3.4.23.-) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14446
R;Pujikura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiFujikura, Y.; Karssen, C.M.
submitted to the EMBL Data Library, January 1994
A;Description: Cauliflower cDNA with sequence homology to gastric proteases.
A;Reference number: S4140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NiAlternate names: aspartyl protease
C;Species: Barasica oleracea (wild cabbage)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S41400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 103; DB 2; Length 292;
Pred. No. 0.014;
9; Mismatches 10; Indels
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hypothetical protein F19K23.21 [imported] - Arabidopsis thaliana
                   Length 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Experimental source: cultivar Alpha Paloma; root tips C, Superfamily: oryzasin; saposin repeat homology C, Keywords: aspartic proteinase; hydrolase
                                                                                                                                                                                     313 VSQCCKTVVDQYGQTILDLLLSETQPKKICSQIGLCT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 SQCKTVVDQXGQTILDLLLSETQPKKICSQIGLCT 135
                                                                                                                                                    43 LSEECQEVVDTYGSSILSILLEEVSPELVCSMLHLCS 79
                                                                                       10;
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                         DB 2;
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A;Accession: T14446
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                         Score 104; DB
Pred. No. 0.02;
                                                                                       10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.0%;
                             25.2%;
                             Query Match 25.2'
Best Local Similarity 45.9'
Matches 17; Conservative
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nes 17; Conservative
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Matches 17; Conservative
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A;Status: preliminary
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-474 <COR>
A;CORS-references: UNIPARC:UPIO00016E005; EMBL:X69193; NID:g499015; PIDN:CAA48939.1; PI
A;Experimental source: flower
C;Superfamily: oryzasin; saposin repeat homology
C;Keywords: aspartic proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: T12049
R;Cordeiro, M.C.; Xue, Z.T.; Pietrzak, M.; Pais, M.S.; Brodelius, P.E.
Biol. 24, 73-741, 1994
A;Title: Isolation and characterization of a cDNA from flowers of Cynara cardunculus end A;Reference number: Z17395; MUID:94250836; PMID:8193298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cjaccesion: F8623
R;Theologis, A.; Beker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., I.J.; J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Recession: F86553
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A,Molecule type: mRNA
A,Residues: 1-428 <COR>
A,Residues: 1-428 <COR>
A,Residues: 1-428 <COR>
A,Crossereferences: UNIPARC:UPI0000175D80; EMBL:X69193
A;Crossereferences: UNIPARC:UPI0000175D80; EMBL:X69193
C;Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent C;Superfamily: oryzasin; saposin repeat homology
C;Keywords: aspartic proteinase; hydrolase
F;236-281/Domain: saposin repeat homology #status atypical <SAP1>
F;230-339/Domain: saposin repeat homology #status atypical <SAP2>
F;23,210/Active site: Asp #status predicted
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C;Species: Cynara cardunculus (cardoon)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar:2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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; Pred. No. 0.012;
10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                   DB 2; Length 428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       43 LSEECQEVVDTYGSSILSILLEEVSPELVCSMLHLCS 79
                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                            25.7%; Score 106; DB 2, 45.9%; Pred. No. 0.011; iive 10; Mismatches
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Best Local Similarity 45.9%;
Matches 17; Conservative 10
                                                                                                                                                                                                                                                                                                                                                45.98;
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Best Local Similarity
Matches 17; Conserv
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C;Species: Arabidopsis thaliana (mouse-ear crees)
C;Accession: B56649
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 815-820, 2000
A;Authors: Hunter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: A86141; MUD:21016719; PMID:11130712
A;Accession: B96649
A;Sterus: preliminary
A;Molecule type: DNA
A;Residues: 1-433 <STO>
A;Cross-references: UNIPROT:004593; UNIPARC:UPI000016DA70; GB:AE005173; NID:g2160151; PI
C;Superfamily: oryzasin; saposin repeat homology
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24.9%; Score 102.5; DB
Best Local Similarity 28.0%; Pred. No. 0.021;
Matches 21; Conservative 18; Mismatches
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; Search time 183.053 Seconds (without alignments) 1257.748 Million cell updates/sec
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Copyright (c) 1993 - 2006 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length DB	DB	ΩI	Description
-	2789	100.0	524	~	AAR70783	Aar70783 Prosaposi
N	2789	100.0	524	~	AAW85652	Aaw85652 Human pro
m	2789	100.0	524	ო	AAY58716	Aay58716 Human pro
4	2789	100.0	524	9	ABU79099	
Ŋ	2789	100.0	524	ø	ABU05200	Abu05200 Human exp
v	2789	100.0	524	9	ABU05207	Abu05207 Human exp
7	2789	100.0	524	9	ABU05203	Abu05203 Human exp
æ	2789	100.0		9	ABU07340	Abu07340 Human exp
6	2789	100.0		ø	ABU05216	Abu05216 Human exp
10	2789	100.0		9	ABU05202	Abu05202 Human exp
11	2789	100.0		9	ABU05214	Abu05214 Human exp
12	2789	100.0	524	9	ABU05215	Abu05215 Human exp
13	2789	100.0		9	ABU05199	Abu05199 Human exp
14	2789	100.0		9	ABU05212	Abu05212 Human exp
12	2789	100.0		9	ABU05213	
16	2789	100.0		9	ABU05205	Abu05205 Human exp
17	2789	100.0		-	ADF43340	Adf43340 Superanti
18	2789	100.0		7	ADJ69401	Adj69401 Human hea
13	2789	100.0		œ	AD008060	Ado08060 Human pol
50	2789	100.0		œ	ADQ94328	Adq94328 Human Pre
21	2789	100.0		œ	ABM81149	Abm81149 Tumour-as
22	2789	100.0		ω	ADS87894	Ads87894 Human pro
23	2789	100.0		œ	ADU48630	Adu48630 Human pro
24	2789	100.0	524	σ	ADW80727	Adw80727 Human pro

Adx06774 Cyclin-de	Ady14302 PRO polyp		Aab31915 Amino aci	Abp68602 Human pan	Abu79100 Lip-TAA b	-	Abu05210 Human exp	Adf43341 Superanti		Abu05211 Human exp	Abu05209 Human exp	Abu05206 Human exp	Adu24090 Human cys	Abr39442 Human GEN	Abr41750 Human DIT	Adb85295 Rat tubul	Abb57102 Mouse isc	Adp29875 Human sec	Ads87898 Human hyp	Aay56966 Human SBP
ADX06774	3 ADY14302	5 ABU05208	1 AAB31915	5 ABP68602	5 ABU79100	5 ABU05204	5 ABU05210	7 ADF43341	1 AAB31916	5 ABU05211	5 ABU05209	5 ABU05206	3 ADU24090	5 ABR39442	5 ABR41750	7 ADB85295	5 ABB57102	3 ADP29875	3 ADS87898	3 AAY56966
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2789	2789	2779	2777.5	2777.5	2777.5	2777.5	2777.5	2777.5	2772.5	2772.5	2768	2767.5	2731	2449.5	2024.5	1969	1921	1293.5	1201	1201
25	26	27	28	29	30	31	32	33	34	35	36	37	38	6	40	41	42	43	4	45

# ALIGNMENTS

98WO-US019216. 97US-0058352P. 98US-0088129P

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(REGC ) UNIV CALIFORNIA.
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on 25-MAR-2003 to correct PN field.) PA field.) (Updated on 25-MAR-2003 to
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cell myelination ex vivo. (Updated (Updated on 25-MAR-2003 to correct correct PI field.)
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Prosaposin is a 70kDa glycoprotein which is proteolytically processed to generate saposins A, B, C and D, all of which are similar to each other and and ave a similar placement of six cysteines, a glycosylation site and conserved proline residues. Prosaposin, saposin C and prosaposin derived conserved proline residues. Prosaposin, saposin C and prosaposin derived conserved proline residues. Prosaposin, saposin C and prosaposin derived conserved proline residues. Prosaposin conserved proline receptor agonists (PRAs) inhibit proinflammatory cytokine-inherited lesions to the pertpheral and central nervous system.

C induced apoptosis by activation of the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2 family members, such as BAD-Bcl-2, releasing Bcl-2 and its family members, such as BAD-Bcl-2, inhibiting apoptosis An additional mechanism whereby PRAs inhibit apoptosis. An additional mechanism whereby PRAs inhibiting apoptosis and its family members which inhibit caspases, thereby inhibiting apoptosis. The activation induced by tumor necrosis factor-alpha (TNF alpha).

C component. Within several minutes after binding to the receptor, PRAs blocking activation of JNK by TNF alpha is another well known mechanism for TNF alpha-induced, as well as other proinflammatory cytokine-induced apoptosis. The method can be used for inhibiting apoptosis and approsicated with a disorder such as even for inhibiting apoptosis associated with a disorder such as even for the second influencephalities, progressive multifocal leukoencephalities, progressive multifocal leukoencephalities, progressive multifocal leukoencephalities, progressive multiple sclerosis, acute disseminated inflammatory disease, fathemic heart disease, dishamatory disease, duillain-Barre disease, traumatic brain disease, duillain-Barre disease, traumatic brain disease, multiple colerosis, duillain-Barre disease, traumatic pluy, raumatic spinal cord injury, alopedis, AlDS demental controlation and disease, multiple sclerosis, duillain-Barre disease,
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100.0%; Pred. No. 4.6e-237;
ive 0; Mismatches 0;
                                                                                                                                                                                            Use of prosaposin receptor agonist
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Best Local Similarity 100.
Matches 524; Conservative
                                                                            WPI; 1999-229139/19.
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                                                                                                                                                                                                                                                                   Prosaponin; saponin B; antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative; antimigratory; Kaposi's sarcoma; tumour;
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VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYLD
                                                                       VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGFCEVCKKLVGYLD
                                                                                                 RNLEKNSTKOBILAALEKGCSFLPDPYOKOCDOFVABYEPVLIBILVEVMDPSFVCLKIG
                                                                                                          PIKKHEVPAKSDVYCEVCEPLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saposin B derived peptides, useful as inhibitors of angiogenesis and
                                                                                                                                                                                                                                                                                                                                 195. .275
/note= "mature saposin B"
195. .205
/note= "specifically claimed antiangiogenic peptide of Claim 23"
196. .200
                                                                                                                                                                                                                                                                                                                                                                    196. .200
/note= "specifically claimed antiangiogenic peptide
Claim 4"
                                                                                                                                   ACPSAHKPLLGTEKCIWGPSYWCONTETAAOCNAVEHCKRHVWN 524
                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                AAY58716 standard; protein; 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertropic scars
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100.0%; Pred. No. 4.6e-237;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 524; Conservative
                                                                                                                                                                                                                                                            Sequence 524 AA;
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30-MAY-2001; 2001US-00870759

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The invention relates to a mammalian cell receptor, useful in the creatment of cancer, which binds to tumour associated lights and induces anergy or apoptosis in the T cells and antigan presenting cells (APCe).

Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds to meet the treatment of cancer where the receptor which binds the deleted or functionally deactivated, producing (MI) a tumouricidal immunocyte appliantolytes in which cellular inactivation or death is deleted or functionally deactivated, producing tumour associated lipids to contact immunocytes in which creeptors for immunosuppressive fatty acids, ceramides, glycolipids, phinopolipids, phosphosphingolipids, gangliosides, sphinopolipids, lipopeptides and protecglycolipids are inactivated or deleted) a construct useful in the treatment of cancer (comprising a lipopeptide inserted into a virus a mammalian T cell useful in the treatment of cancer (comprising a lipid tate conjugated to a superantigen (SAg nucleotal immunocyte population asful in the treatment of cancer (comprising a lipid and tate of the contact immunocytes, in which cancer (comprising a lipid at the conjugated to a superantigen), producing (M) a tumouricidal immunocyte population, and administering the tumouricidal immunocyte population, and administering the tumouricidal immunocytes population, and administering the tumouricidal oppulation of vivo in a mammal loy allowing a tumouricidal of context APCe, in which redeptors for the tumouricidally activated published to context APCe, in which adaptor proteins, which inhibit T cells and administering the tumour associated antigens of context colls to produce a tumouricidally activated T cells to the host, or administering the tumour associated antigens or context cells activated or deleted or produce a tumouricidal population in vivo in a mammal loy allowing a tumouricidal T cells of unduringential presention in vivo in a mammal context cells activated or cells evivor and administering the tum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the printed specification, but was obtained in electronic format from the US patnet office website at
                                                                                                                                                                                                                mammalian cell receptor, useful in the treatment of cancer by binding tumor associated lipids where the binding induces anergy or apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion constructs with anti-tumour proteins or motifs. The present sequence represents a tumour antigen or a motif identifying a tumour antigen, which can be functionally deactivated in the method of the invention. Note: The sequence data for this parent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             segdata.uspto.gov/sequence.html?DocID=20020177551"
                                                                                                                                                                                                                                         to tumor associated lipids where the bir
in T cells and antigen presenting cells.
                                                                                                                                                                                                                                                                                                      Disclosure; Page; 167pp; English
                                        31-MAY-2000; 2000US-0208128P.
                                                                                                                                                                         WPI; 2003-361759/34
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Length 524; 100.0%; Score 2789; DB 6; ilarity 100.0%; Pred. No. 4.6e-237; Conservative 0; Mismatches 0; Best Local Similarity Matches 524; Conserv Sequence 524 AA; Query Match

Urban RG;

Tomlingon AJ,

Chicz RM,

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WPI; 2003-040607/03

120 180 300 420 480 Translational profilling; expressed protein tag; BPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MTC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia. 120 180 240 240 9 61 LPCDICKDVVTAAGDMLKONATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDEVKEMPMQTLVPAKVASKNVIPALELUB 361 VDIYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGPCEVCKALVGYLD 61 LPCDICKDVVTAAGDMLKDNATEEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 121 IKGEMSRPGEVCSALNLCESLOKHLAELNHOKOLESNKIPELDMTEVVAPFMANIPLLLY PODGPRSKPOPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADI CKNYISQYSEIAIQMMMHMQPKEICALVGFCDBVKEMPMQTLVPAKVASKNVIPALELVE PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKBILDAFDKMCSKLPKSLSBECQEV VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYLD RNLEKNSTKOEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIBILVEVMDPSFVCLKIG ACPSAHKPLLGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN 524 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN 524 Human expressed protein tag (BPT) #1866. ABU05200 standard; protein; 524 AA 28-MAR-2001; 2001US-0279495P. 21-MAY-2001; 2001US-0292544P. 08-AUG-2001; 2001US-0310801P. 04-DCC-2001; 2001US-0326370P. 04-DEC-2001; 2001US-0336780P. 20-PEB-2002; 2002US-0358985P. 28-MAR-2002; 2002WO-US009671 29-JAN-2003 (first entry) (ZYCO-) ZYCOS INC WO200278524-A2. Homo sapiens. 10-OCT-2002. 481 301 301 361 181 421 RESULT 5 ABU05200 ID ABU0 셤 셤 요 셤 ò g g ò 요 δ ò δ Š Š 셤 ઠ

profiling; expressed protein tag; EPT; kinase; phosphatase;

Human expressed protein tag (RPT) #1873.

Translational

(first entry)

29-JAN-2003

ABU05207;

protease; protease inhibitor; transporter; cyfoskeletal protein; receptor; transcription factor; cancer; wHG; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

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the invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MRC-binding polypeptide. The polypeptides and plymucleotides are particularly useful for treating or preventing or preventing myeloma, colon cancer, gastric cancer, reating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an treating the above mentioned diseases. This sequence represents an profilling. Note: This sequence does not appear in the printed grown WIPO at apecification but was obtained in electronic format directly from WIPO at
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100.0%; Pred. No. 4.6e-237;
tive 0; Mismatches 0;
   New polypeptides (e.g. kinases, phosphatases, cytoskeletal proteins, receptors or transcript
                                                                                                                                                                      Example 2; SEQ ID NO 1866; 134pp; English
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Matches 524; Conservative
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8 셤 ò 셤 ઠે 윱 ઠે 셤 ò 셤 ò g δ 원

Urban RG;

Tomlinson AJ,

Chicz RM,

(ZYCO-) ZYCOS INC.

WPI; 2003-040607/03.

21-MAY - 2001; 2001US-0292544P 08-AUG-2001; 2001US-0310801P 01-CCT-2001; 2001US-0326370P 04-DBC-2001; 2001US-0358985P.

28-MAR-2002; 2002WO-US009671

28-MAR-2001;

WO200278524-A2.

10-OCT-2002

Homo sapiens.

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fragment of a kinase, phosphatase, protease inhibitor, fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskelatal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and compounds that binds to a sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an treating the above mentioned diseases. This sequence represents an profiling. Note: This sequence does not appear in the printed profile the compound of the compound of the printed format directly from WIPO at the printed for the compound of the printed format directly from WIPO at the compound of the compound
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ABU05207 standard; protein; 524 AA.

ABU05207 ID ABU0 XX RESULT 6

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transporter, cytoskeletal protein, troceptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic composition for eliciting in a cammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to polypeptide. The purified polypeptide, or the antibody that binds to the purified polypeptide, or treating cancer. The polypeptide is also polypeptide, is useful for treating compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polymentic cancer, adenocarionan, melanoma, myeloma, colon cancer, gastric cancer, adenocarionan, astrona, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an profiling. Note: This sequence does not appear in the printed from WIPO at gpecification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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                                                                                                               CKNY I SOY SEI A I OMMHIMO PKEI CALVG F CDEVKEM PMOTL V PAKVASKNV I PALELVE
                                                                                                                                                                             PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEV
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                                                                                                                                                                                                                                                                                                       RNLEKNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG
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                                                                                                                                                                                                                                                                                                                                                                                   ACPSAHKPLIGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human expressed protein tag (EPT) #1869
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21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
01-OCT-2001; 2001US-0326370P.
04-DEC-2001; 2001US-0336780P.
20-PEB-2002; 2002US-03589965P.
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for treating cancer. The polypeptide is also useful for treating polypeptide. The polypeptide is also useful for binds to a naturally processed class I or class II MiC-binding polypeptide. The polypeptides and polymucleotides are particularly useful for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Translational profiling, expressed protein tag, EPT; kinase, phosphatase, protease, protease inhibitor; transporter; cytoskeletal protein; reseptor; transcription factor; cancer; WHG; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                                                                                                               New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for
                                                                                                                                                       VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYLD
CKNYISQYSEIAIQMMHMQPKEICALVGFCDEVKEMPMQTLVPAKVASKNVIPALELVE
                                        PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEV
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21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
04-DEC-2001; 2001US-033570P.
04-DEC-2001; 2001US-0336780P.
20-FBB-2002; 2002US-0358985P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this cuseful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptide is also cuseful for class II MHC-binding polypeptide. The polypeptides and polymentical cancer, adenocarcinoma, sarcoma, melanoma, clon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, clumphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein age (BFP) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed companied in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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         complex; myeloma; colon cancer; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma o
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                               adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Urban RG;
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21-MAY-2001; 2001US-0295544P.
08-AUG-2001; 2001US-0316801P.
01-DCCT-2001; 2001US-0336370P.
04-DEC-2002; 2001US-0336780P.
20-FEB-2002; 2002US-03589965P.
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      histocompatability
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New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

treating

leukemia

RG Urban

Chicz RM, Tomlingon AJ, WPI; 2003-040607/03

(ZXCO-) ZXCOS

; 2001US-0279495P. ; 2001US-032544P. ; 2001US-0310801P. ; 2001US-0336730P. ; 2002US-0358985P.

21-MAY-2001; 08-AUG-2001; 01-OCT-2001; 04-DEC-2001; 20-FEB-2002;

2002WO-US009671

28-MAR-2002;

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myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expenseed protein tag (EPT) isolated from human tissue for translational profilling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
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; Pred. No. 4.6e-237;
0; Mismatches 0;
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                                                                                                                                                                  al Similarity 100.
524; Conservative
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Best Local S
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phospharase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The transporter is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified of polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide. The useful for traating cancer. The polypeptide is also cuseful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polymenticleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, claukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an concerning and the above mentioned diseases. This sequence for translational concerning the above mentioned diseases. This sequence does not appear in the printed profiling. Note: This sequence does not appear in the printed from WIPO at the wipo.int/pub/published_pct_sequences
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100.0%; Pred. No. 4.6e-237;
tive 0; Mismatches 0;
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Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease; inhibitor; transporter; cytoskeletal protein; reseptor; transcription factor; cancer; MTC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
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100.0%; Score 2789; DB 6;
100.0%; Pred. No. 4.6e-237;
ive 0; Mismatches 0;
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21-MAY-2001; 2001US-0292544F.
08-AUG-2001; 2001US-0310801P.
04-DEC-2001; 2001US-0326370F.
04-DEC-2001; 2001US-0336780F.
20-FEB-2002; 2002US-0356985F.
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    Query Match
Best Local Similarity 100.
Matches 524; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Translational profiling, expressed protein tag, EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; reseptor; transcription factor; cancer; WHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
            RNLEKNSTKOEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
                                 New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                             ACPSAHKPLIGTEKCIWGPSYWCONTETAAQCNAVEHCKRHVWN 524
                                                                                                   ACPSAHKPLLGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN
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21-MAY-2001; 2001US-0295544P.
08-AUG-2001; 2001US-0316801P.
01-OCT-2001; 2001US-0336370P.
04-DEC-2001; 2001US-0336780P.
20-FEB-2002; 2002US-0358985P.
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ABU05199 standard, protein, 524
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100.0%; Pred. No. 4.6e-237;
tive 0; Mismatches 0;
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ses 524; Conservative
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(ZYCO-) ZYCOS INC
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I transporter, cytoakeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polymucleotides are particularly useful for treating or preventing polymucleotides are particularly useful for treating or preventing compounds that binds to a screening agents for treating the above mentioned diseases. This sequence represents an treating the above mentioned diseases. This sequence for translational profiling. Note: This sequence does not appear in the printed profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                         Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MTC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
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Human expressed protein tag (EPT) #1865.
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21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
04-DEC-2001; 2001US-0326370P.
04-DEC-2001; 2001US-035698PP.
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Matches 524; Conservative
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21-MAY-2001; 2001US-0292544P.
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01-OCT-2001; 2001US-033679P.
04-DEC-2001; 2001US-0336780P.
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified onlypeptide. The purified polypeptide, or the antibody that binds to the purified polypeptide, is useful for transing cancer. The polypeptide is also conformed that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides are particularly useful for treating or preventing polymucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, Irmanema or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents and treating the above mentioned diseases. This sequence represents concernated profiling. Note: This sequence does not appear in the printed from WIPO at the wipo.int/pub/published_pct_sequences
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Pred. No. 4.6e-237;
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Example 2; SEQ ID NO 1878; 134pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment of a kinase, phosphatase, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide is useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polymuleotides are particularly useful for treating or preventing myeloms, colon cancer, adenocarcinoms, asrcoma, melanoms, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an treating the above mentioned diseases. This sequence represents an profiling. Note: This sequence does not appear in the printed profiling to but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPCDICKDVVTAAGDMLKDNATBEBILVYLEKTCDWLPKPNMSASCKBIVDSYLPVILDI 120
                                       Translational profiling, expressed protein tag, BPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; transcription factor; cancer; WHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPCDICKDVVTAAGDMLKDNATEEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI
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Pred. No. 4.6e-237;
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100.0%; Pred. No. ...
0; Mismatches
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Human expressed protein tag (EPT) #1879.
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2001US-0292544P.
2001US-0310801P.
2001US-0326370P.
2001US-0336780P.
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04-DEC-2001; 2001US-0336780P
20-PEB-2002; 2002US-0358985P
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CKNYISQYSEIAIQMMAHMQPKEICALVGPCDEVKEMPMQTLVPAKVASKNVIPALELVE
                                                                                      PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKBILDAFDKMCSKLPKSLSEECQEV
                                                                                                      361 VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYLD
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Search completed: January 13, 2006, 16:30:19 Job time : 186.053 secs

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2006
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OM protein - protein search, using sw model

Run on:

January 13, 2006, 16:23:49; Search time 41.6424 Seconds (without alignments) 1210.728 Million cell updates/sec

US-10-801-517-1 2789 score:

1 MYALFILASILGAALAGPVL......NTETAAQCNAVEHCKRHVWN 524 Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283416 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	saposin precursor		saposin precursor	Pl09 protein - sil	cerebroside sulfat	pulmonary surfacta		saposin-C - bovine		surfactant protein	glucosylceramide b	pulmonary surfacta	hypothetical prote		hypothetical prote		hypothetical prote	aspa			cyprosin (EC 3.4.2	aspartic proteinas	•	aspartic proteinas			Ω	protein T08A9.7 [1	B-selectin ligand-
SUMMARIES	QI	SAHUP	A28716	JH0604	T00207	A49475	S02766	LINHUB	S21770	A29072	146531	A32026	LINRBB	T46069	T48201	T15677	T09739	F86253	T07915	T11686	S47096	T12049	S19697	T15674	T14446	S41400	JS0732	JC7272	ထ	852417
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dif	Ouery Match	9.66	71.6	69.5	18.3	13.9	13.6	12.5	12.3	11.1	10.8	4.6	9.5	7.6	7.3	6.3	6.2	6.1	5.9	5.8	ю. 89	5.8	5.7	5.6	2.6	5.6	5.5	5.5	5.2	5.1
••	Score	2777.5	1996	1937.5	511	389	379	348.5	. 343	310	301.5	261	256.5	213	203.5	176.5	173.5	171.5	165.5	161.5	161	161	158.5	156	155.5	155.5	154	153.5	145.5	143.5
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5.1	5.1	5.1	5.1	4.8	4.8	4.6	4.6	4.5	4.5	4.5	4.4	4.3	4.2	4.2	4.2
142.5	142.5	142.5	141	134	132.5	127.5	127.5	126.5	126.5	126	123.5	119	116.5	116.5	116
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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ESULT	AHUP	

Saposin precursor [validated] - human
N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component
sin (SAP); sphingolipid activator protein A2; sulfatide sulfatase activator protein
N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D
C; Species: Homo sapiens (man)
C; Date: 30-Jun-1992 #sequence\_revision 17-Nov-1995 #text\_change 09-Jul-2004
C; Accession: JV0661; AB7368; A2003; B42003; D42003; D42003; A30367; S34740; S36140; S36
D226; I37265; I37264
R;Makano, T.; Sandhoff, K.; Stuemper, J.; Christomanou, H.; Suzuki, K.
J. Biochem. 105, 152-154, 1989
A;Title: Structure of full-length cDNA coding for sulfatide activator, a Co-beta-glucosi
A;Reference number: JX0061; MUID:89255151; PMID:2498298

A;Molecule type: mRNA A;Residues: 1-527 ANAK. A;Cross-references: UNIPROT:P07602; UNIPARC:UPI000002B33D; GB:D00422; NID:g220063; PIDN A;Note: alternative splice form 1

A; Accession: A57368

A; Molecule type: mRNA A; Residues: 1.259,263-527 <NA2> A; Cross-references: UNIPARC: UP1000000DBP; GB:J03015; GB:J03086; NID:g337755; PIDN:AAB59 A; Note: alternative splice form 2 R; Rorman, E.G.; Scheinker, V.; Grabowski, G.A. Genomics 13, 312-318, 139. A; Title: Structure and evolution of the human prosaposin chromosomal gene. A; Reference number: A42003; MUID:92307663; PMID:1612590

A; Accession: A42003

A;Molecule type: DNA A;Residues: 50-140 <ROR> A;Cross-references: UNIPARC:UP100001741AA; GB:M86181 A;Mote: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107236) A;Accession: B42003

A, Molecule type: DNA

A;Residues: 185-259;263-276 <RO2> A;Cross-references: UNIPARC:UPI00001741AB; UNIPARC:UPI00001741AC A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107237)

A; Molecule type: DNA

A; Residues: 305-393 <RO3>

A;Cross-references: UNIPARC:UP100001741AD A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107238); sequence inc A;Accession: D42003

A; Molecule type: DNA
A; Residues: 399-487 <RO4>
A; Residues: 399-487 <RO4>
A; Cross-references: UNIPARC:UPI00001741AB
A; Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107239); sequence inc
Genomics S; 486-492, 1989
A; Title: Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sphin
A; Reference number: A30367; MUID:90129043; PMID:2515150

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A; Accession: S13196
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 'XXX',413-414,'X',416-428,'X',430-434 <TY2>
A; Cross-references: UNIPARC:UP100001741B4
A; Notes saposin D
B; Holtechmidt, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K.
B; Holtechmidt, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K.
B; Holtechmidt, H.; Sandhoff, M.J.
J. Biol. Chem. 266, 7556-7560, 1991
A; Title: Sulfatide activator protein. Alternative splicing that generates three mkNA a; Accession: S36988; MUID:91210267; PMID:2019586
A; Accession: S36988
A; Accession: S36988
A; Residues: 1-240,'S', A42-527 <HOL'
A; Residues: 1-240,'S', A42-527 <HOL'
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A; Note: cerebroside sulfate activator protein mutant MU-9; corresponds to alternative sp
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A; Residues: 1-240,'S'. 242-259,261-527 <HO3>
A; Residues: 1-240,'S'. 242-259,261-527 <HO3>
A; Cross-references: UNIPARC: UPIO00016AFF8; EMBL: M60258; NID:9337766; PIDN: AAA36596.1; PI A; Cross-references: UNIPARC: UPIO00016AFF8; EMBL: Multimet MU-6; Corresponds to alternative BF, Note: cerebroside sulfate activator protein mutant MU-6; corresponds to alternative BF, Kondoh, K.; Hineno, T.; Sano, A.; Kahmoto, Y.
B; Kondoh, K.; Hineno, T.; Sano, A; Kahmoto, Y.
B; Kondoh, K.; Hineno, T.; Sano, A; Kahmoto, Y.
A; Pitle: Isolation and characterization of prosaposin from human milk.
A; Pitle: Isolation and characterization of prosaposin from human milk.
A; Reference number: PS0330; MUID: 92068206; PMID: 1958198
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A; Molecule type: protein
A; Residues: 17-24, X, 26 < KCON>
A; Experimental source: milk
B; Kretz, K, A: 0 farson, G.S.; Morimoto, S.; Kishimoto, Y.; Fluharty, A.L.; O'Brien, J.S.
Proc. Natl. Acad. Sci. U.S.A. 87, 2541-2544, 1990
Proc. Natl. Acad. Sci. U.S.A. 87, 2541-2544, 1990
A; Title: Characterization of a mutation in a family with saposin B deficiency: a glycosy
A; Reference number: A35985; MUID:90207231; PMID:2320574
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    A;Cross-references: UNIPARC;UPI000000DBF; GB:J03077; NID:g183230; PIDN:AAA52560.1; PID: A;Note: alternative splice form 2
A;Note: alternative splice form 2
R;Hiraiwa, M.; O'Brien, J.S.; Kitahimoto, Y.; Galdzicka, M.; Fluharty, A.L.; Ginns, E.I.; Arch. Blochem. Blochem. 3104, 110-116, 1993
A;Hitle: Isolation, characterization, and proteolysis of human prosaposin, the precursor A;Reference number: 834740; MUD:93311991; PMID:8323276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 17-2;180-189;301-305 (HIR)
A; Cross-references: UNIPARC:UF100001741AF; UNIPARC:UF100001741B1;
A; Cross-references: UNIPARC:UF100001741AF; UNIPARC:UF100001741B1;
A; Tymelae, 7; Palmer, D.N.; Baumann, M.; Haltia, M.
FEBS Lett. 330, 8-12, 1993
A; Mittle: Storage of saposins A and D in infantile neuronal ceroid-lipofuscinosis.
A; A; Reference number: 836140; MUID:93380576; PMID:8370464
A; Accession: 836140
A; Molecule type: protein
A; Residues: 'XX', 62, 'X', 64-65, 'X', 67-79, 'X', 81-84 <TYY>
A; Cross-references: UNIPARC:UF100001741B3
A; Note: saposin A
A; Accession: 836141
A; Accession: 836141
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A.Residues: 1-240, 'S', 242-259, 263-527 <HO2>
A.Cross-references: UNIPARC:UPI000016AFF7; EMBL:M60257; NID:g337764; PIDN:AAA36595.1;
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A.Note: cerebroside suffate activator protein mutant MU-0; corresponds to alternative
A.Accession: S36990
A.Status: mucleic acid sequence not shown; translation not shown
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A;Molecule type: mRNA
A;Residues: 1-259,263-527 <KR2>
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A;Residues: 213-221 <KRE>
A;Cross-references: UNIPARC:UP100001741B6; GB:M32221
A,Molecule type: mRNA
A,Residues: 1-259,263-527
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A) Experience and the control of the
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MyAlternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component NyAlternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfata N;Contains: prosaposin; saposin B; saposin B; saposin D; saposin D; cjspecies: Mus musculus (house mouse)
Cjspecies: Nus musculus (house mouse)
Cjoate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
CjAccession: JH0604
B;Tsuda, M.; Sakiyama, T.; Endo, H.; Kitagawa, T.
Biochem. Biophys. Res. Commun. 184, 1266-1272; 1992
A;Title: The primary structure of mouse saposin.
A;Reference number: JH0604; MUID:92272718; PMID:1590788
        C;Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome; F;1-56/Domain: signal sequence #status predicted <SIG>F;1-554/Product: prosaposin #status predicted <PRO>F;55-148/Domain: saposin repeat homology <SAPI>F;60-143/Product: saposin R #status predicted <SAPA>F;189-280/Domain: saposin R #status predicted <SAPA>F;189-280/Domain: saposin R #status predicted <SAPI>F;180-280/Domain: saposin R #status predicted <SAPI>F;30-397/Domain: saposin repeat homology <SAPI>F;30-397/Domain: saposin repeat homology <SAPI>F;30-389/Product: saposin R #status predicted <SAPI>F;310-389/Product: saposin D #status predicted <SAPI>F;310-389/Product: saposin D #status predicted <SAPI>F;31-524/Product: saposin D #status predicted <SAPI>F;31-514/Product: saposin D #status predicted <SAPI>F;31-314/Broduct: saposin C #status predicted <SAPI-314/Broduct: saposin D #status predicted <SAPI-31314/Broduct: saposin D #status predicted F;30,2131456/Binding site: carbohydrate (Ash) (covalent) #status predicted F;80,214,331,456/Binding site: carbohydrate (Ash) (covalent) #status predicted F;197-270,200-264,229-240,314-387,317-381,345-356/Disulfide bonds: #status predicted
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66.3%; Pred. No. 4.2e-124;
ive 77; Mismatches 78;
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Matches 368; Conservative
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NiAlternate names: carebroside sulfate activator protein; co-beta-glucosidase; component
ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfate
NiContains: prosaposin, saposin A3; saposin C; saposin D;
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Name of Saposin A2; saposin D;
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A28716
R;Collard, M.W.; Sylvester, S.R.; Tsuruta, J.K.; Griswold, M.D.
Biochemistry 27, 4557-4564, 1988
A;Title: BioSynthesis and molecular cloning of sulfated glycoprotein 1 secreted by rat E
Biochemistry 27, 4557-4564, 1988
A;Title: BioSynthesis and molecular cloning of sulfated glycoprotein 1 secreted by rat E
A;Reference number: A28716
A;Accession: A28716
A;Access
                                                                                                                                             PID
                                                A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 59-125 <RES>
A;Cross-references: UNIPARC:UPI000016A751; EMBL:XS7107; NID:g30234; PIDN:CAA40391.1;
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                                                                                                                                                                                       Query Match
99.6%; Score 2777.5; DB 1; Length 527;
Best Local Similarity 99.4%; Pred. No. 1.1e-175;
Matches 524; Conservative 0; Mismatches 0; Indels 3;
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A;Reference number: 137264; MUID:91192146; PMID:2013321
A;Accession: 137265
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A;Accession: unvolva
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT: Q61207; UNIPARC: UP10000170C25; GB:S36200; NID: 9249386; PIDN:
A;Cross-references: UNIPROT: Q61207; UNIPARC: UP10000170C25; GB:S36200; NID: 9249386; PIDN:
A;Experimental source: liver
C;Function: saposins bind sphingolipids, form hydrophilic complexes and make them acc
A;Description: saposins and C (SAP-2) activate hydrolysis of galactocerebroside by beta-glucosy
A;Dote: saposins A and C (SAP-2) activates hydrolysis of galactocerebroside sulfate by arylsulf
A;Note: saposin B (SAP-1) activates hydrolysis of sphingomyelin by sphingomyelin phosphodiestera
A;Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiestera
A;Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiestera
C;Superfamily: saposin repeat homology
C;Superfamily: saposin R #status predicted <SAPO>
F;1-16/Domain: saposin Repeat homology <SAPO>
F;194-276/Product: saposin repeat homology <SAPO>
F;305-400/Domain: saposin Repeat homology <SAPO>
F;305-138,66-132,94-106,197-273,200-287,229-240,317-390,320-384,348-359,442-515,445-509,4
F;60-138,66-132,94-106,197-273,200-287,229-240,317-390,320-384,348-359,442-515,445-509,4
F;80,214,334,379,459/Binding site: carbohydrate (Asn) (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                             Length 557;
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                               69.5%; Score 1937.5; DB 1
63.6%; Pred. No. 3.1e-120;
tive 77; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETAAQCNAVEHCKRHVWN 524
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Matches 355; Conservative
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priog protein - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00207
Gene 212, 287-293, 1998
A;Title: Molecular cloning of a cDNA encoding a silkworm protein which contains the conse
A;Title: Molecular cloning of a cDNA encoding a silkworm protein which contains the conse
A;Title: Molecular cloning of a cDNA encoding a silkworm protein which contains the conse
A;Accession: T00207
A;Accession: T00207
A;Residues: L-965 <TAM>
A;Residues: L-965 <TAM>
A;Cross-references: UNIPROT:015997; UNIPARC:UPI000007B54A; EMBL:AB008449; NID:g2575864; F
P;778-870/Domain: saposin repeat homology <SAP3>
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Cerebrosides Sus scrofa domestica (domestic pig)

C;Species: Sus scrofa domestica (domestic pig)

C;Species: 24-Peb-1994 #sequence_revision 18-Nov-1994 #text_change 17-May-1996

C;Accession: A49475

C;Accession: A49475

Biochemistry 32, 4051-4059, 1993

A;Itle: Porcine cerebroside sulfate activator: further structural characterization and

A;Reference number: A49475; MUID:93229506; PMID:8471613

A;Accession: A49475

A;Status: preliminary

A;Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALELVE--PIKKHRVPA-KSDVYÇEVÇEFLVKEVIKLIDNNKTEKBILDAFDKMÇSKLPK 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 NIÇES--LOKHLAELNHOKOLES------NKI PELDWTEVVAPFMA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 VLGLKECTRGSAVWCQNVKTASDCGAVKHCLOTVWNK---PTVKSLPCDICKDVVTAAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 965;
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18.3%; Score 511; DB 2; Length 96
Best Local Similarity 24.6%; Pred. No. 7.5e-26;
Matches 139; Conservative 104; Mismatches 229; Indels
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pulmonary surfactant protein B precursor [validated] - human N;Alternate names: pulmonary surfactant-associat C;Species: Homo sapiens (man) (man) C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text change 09-Jul-2004 C;Accession: A31361; A28461; A27794; A27592; JU0162; S21134 A31361; A28461; A27794; A27592; JU0162; S21134 A31361; A28461; A2846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 'EFR', 99-317, 'L', 319-381 <GLA>
A; Residues: 'EFR', 99-317, 'L', 319-381 <GLA>
A; Cross-references: UNIPARC:UP1000014237D; GB:M16764; NID:g338410; PIDN:AAA88099.1; PID
A; Cross-references: UNIPARC:UP1000014237D; GB:M16764; NID:g338410; PIDN:AAA88099.1; PID
A; Note: 131-11e was also found
A; Note: bart of this sequence, including the amino end of the mature protein, was confi
B; Revak, S.D.; Merritt, T.A.; Degryse, E.; Stefani, L.; Courtney, M.; Hallman, M.; Coch
J, Clin. Invest. 81, 826-833, 1988
A; Title: Use of human surfactant low molecular weight apoproteins in the reconstitution
A; Reference number: A27592; MUID:88139786; PMID:3343343
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A; Residues: 139-177, VV, 179-227, AV, 228-381 <REV>
A; Residues: 139-177, VV, 179-227, AV, 228-381 <REV>
A; Cross-references: UNIPARC: UPI00001741A7; GB: M19097
A; Note: part of this sequence, including the amino end of the mature protein, was confi A; Note: the mature protein (SP 18) consists of two identical disulfide-bonded 9K polype R; Mizumoto, M.; Adachi, H.
Sapporo Igaku Zasshi S6, 731-742, 1987
A; Title: Primary structure of a hydrophobic 6KDa apoprotein (SP6) of human pulmonary su A; Reference number: JU0162
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A;Residues: 201-207,'X',209-210,'X',212-227,'A',229-234,'X',236-245,'X',247,'L',249-253
A;Cross-references: UNIPARC:UPI00001741A8
R;Johansson, J; Joernvall, H; Curstedt, T.
PEBS Lett. 301, 165-167, 1992
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A;Reference number: S21134; MUID:92233937; PMID:1568474
                                    293 ECHFCKSVI-----NQAWNISEQAMPQAMHQACLRFWLD--RQKCEQFVEQHMPQLLALV 345
408 FCEVCKKLVGYLDRNLEKNSTKQEILAALEKGC-SFLPDPYOKQCDQFVAEYBPVLIEIL
                                                                                                                                                       467 VEVMDPSFVCLKIGACPSAHKPLLGTEKCIWGP 499
                                                                                                                                                                                                                             346 PRSQDAHTSCQALGVCBAPASPL----QCFQTP 374
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A;Residues: 201-227,'I','229-279 <JOH>
A;Cross-references: UNIPARC:UP100001741A9
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Ribarie, P.A.; Shannon, J.M.; Mason, R.J.; Fisher, J.H.
Biochim. Biophys. Acta 994, 215-221, 1998
Biochim. Biophys. Acta 994, 215-221, 1998
A;Title: CDNA and deduced amino acid sequence for the rat hydrophobic pulmonary surfacts
A;Reference number: S02766; MUID:89150284; PMID:2920185
A;Accession: S02766
A;Molecule type: mRNA
A;Residues: 1-376 cEMR>
A;Residues: 1-376 cEMR>
A;Cross-references: UNIPROT:P22355; UNIPARC:UPI00001327F8; EMBL:X14778; NID:957284; PIDN
C;Superfamily: pulmonary surfactant protein B; saposin repeat homology
F;1-19/Domain: saposin repeat homology cSAR1>
F;59-151/Domain: saposin repeat homology cSAR2>
F;191-277/Domain: saposin repeat homology cSAR2>
F;191-269/Product: pulmonary surfactant protein B #status predicted cMAT>
F;286-371/Domain: saposin repeat homology cSAR3>
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                                                                                                                                                                                                                                                                                                                                                                                                    195 GDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADICKNYISQYSEIAIQ 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 YISQYSBIAIQMMMHMQPKBICALVGFCDBVKEMPMQTLVPAKVASKNVIPALE---LVB 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----MLDAIPNPLLNKLVLPALPGAFLAR 178
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 PGPHTQDLSEQQLPIPLP-FCWLCRTLIKRVQAVI----PKGVLAVAVSQVCHVVPLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GDVCQDCIQWYTDLQNAVRTNSTFVEALVNHAKEECDRLGPGWADMCKNYISQYSEIAIQ
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Best Local Similarity 22.6%; Pred. No. 1.2e-17;
Matches 116; Conservative 75; Mismatches 158; Indels 164; Gaps
                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                         Length 79,
                                                                                                                                                                                                                                         Query Match 13.9%; Score 389; DB 2; Length 79
Best Local Similarity 88.6%; Pred. No. 3.6e-19;
Matches 70; Conservative 5; Mismatches 4; Indels
A,Cross-references: UNIPARC:UPI0000177938
A,Experimental source: kidney
A,Note: sequence extracted from NCBI backbone (NCBIP:129597)
C,Superfamily: saposin; saposin repeat homology
F;1-79/Domain: saposin repeat homology
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A;Note: 228-Ala was also found
C;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers t
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Cross-references: GDB:120374; OMIM:178640
A;Map position: 2p12-2p11.2
B;19-13/Domain: saposin repeat homology cARP2>
F;201-256/Product: pulmonary surfactant protein B, K form #status predicted cSP6>
F;201-256/Product: pulmonary surfactant protein B, K form #status predicted cSP6>
F;201-256/Product: pulmonary surfactant protein B, K form #status predicted cSP6>
F;201-376/Domain: saposin repeat homology cSAP3>
F;201-377,101-271,235-246/Disulfide bonds: #status spredicted
F;248/Disulfide bonds: interchain #status experimental
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R;Sano, A.; Mizuno, T.; Kondoh, K.; Hineno, T.; Ueno, S.; Kakimoto, Y.; Morita, N.
Bjochim. Biophys. Acta 1120, 75-80, 1992
A;Title: Saposin-C from bovine gpleen; complete amino acid sequence and relation between
A;Reference number: S21770; MUID:92207994; PMID:1554743
                                                                                                                                                                                                                                    T
T
                               Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 QDGPRSKPQPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADIC 241
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C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 YALFLLASLIGAALAGPVLGLKECTRGSAVWCONVKTASDCGAVKHCLQTVWNKPTVKSL
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Best Local Similarity 21.6%; Pred. No. 1.2e-15;
Matches 111; Conservative 72; Mismatches 171; Indels 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVPRGWDAHTTCQALGVCGTMSSPL----QCIHSP 379
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A;Cross-references: UNIPROT: P17129; UNIPARC: UP10001327F3; GB:M15170; NID:g164077; PIDN: A;Accession: A29072
A;Abccession: A29072
A;Rocidus: 182-210 cHA2>
A;Cross-references: UNIPARC: UP1000177937
A;Cross-references: UNIPARC: UP1000177937
F:1-14/Domain: signal sequence #status predicted cSIG>
F:1-180/Domain: propeptide #status nredicted cSIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pulmonary surfactant protein SP 18 precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: B29072; A29072
R;Hawgood, S.; Benson, B.J.; Schilling, J.; Damm, D.; Clements, J.A.; White, R.T. Proc. Natl. Acad. Sci. U.S.A. 84, 66-70, 1987
A;Title: Nuclectide and amino acid sequences of pulmonary surfactant protein SP 18;A;Reference number: A29072; MUID:87092398; PMID:3467361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNMSASCKBIVDSYLPVILDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 IKGEMSRPGEVCSALNICESLOKHLAELNHOKOLESNKIPELDMTEVVAPPMANIPLLLY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99T AGATON 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 CKNYISQYSEIAIQMMMHMQPKBICALVGFCDEVKEMPMQTLVPAKVASKNVIPALELVR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Superfamily: pulmonary surfactant protein B; saposin repeat homology F;1-14/Domain: signal sequence #status predicted <SIG> F;1-180/Domain: saposin repeat homology <SAPI> F;54-146/Domain: saposin repeat homology <SAPI> F;180-267/Domain: saposin repeat homology <SAPI> F;181-363/Product: pulmonary surfactant protein SP 18 #status experimental F;273-358/Domain: saposin repeat homology <SAPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFLLASL--LGAA-LAGPVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                  311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 FQSQIN-PKIICKHLGLC---KPGLPEPEQESELSDPLLDKLILPEL
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                                                                                                                                                                                              9
                                                                                                                                              12.3%; Score 343; DB 2; 79.7%; Pred. No. 3.9e-16; tive 10; Mismatches 6;
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-80 cSAN-
A;Cress-references: UNIPARC:UDI000177939
C;Superfamily: saposin; saposin repeat homology
                                                                                                                                                                                                                                                                                                                                                         371 ILLEEVSPELVCSMLHLCS 389
                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                      169 TGPHTQDLSE------
                                                                                                                                                   Query Match 12.3% Best Local Similarity 79.7% Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 22.0°
Matches 112; Conservative
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A, Residues: 1-363 <HAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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Glucosylceramide beta-glucosidase activator protein SAP-2 - guinea pig
Glypecies: Cavia porcellus (guinea pig)
Glypecies: Cavia porcellus (guinea pig)
Glypecies: Or-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
Glycesesion: A32026
Fisano, A.; Radin, N.S.; Johnson, L.L.; Tarr, G.E.
J. Biol. Chem. 263, 19597-19601, 1988
A;Title: The activator protein for glucosylceramide beta-glucosidase from guinea pig li*
A;Reference number: A32026; MUID:89066787; PMID:3198642
A;Reference number: A32026
A;Residues: 1-81 <SAN>
A;Residues: 1-81 <SAN
A;Crosser-references: UNIPROT:P20097; UNIPARC:UP1000013555A
G;Superfamily: saposin; saposin repeat homology <SAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: A32421
R;Xu, J.; Richardson, C.; Ford, C.; Spencer, T.; Li-juan, Y.; Mackie, G.; Hammond, G.; Isochem. Biophys. Res. Commun. 160, 325-332, 1989
A;Title: Isolation and characterization of the cDNA for pulmonary surfactant-associated A;Reference number: A32421; MUID:89228033; PMID:2469419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alfocusiani, 13-10.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 DICKDVVTAAGDMLKDNATEEEILVYLEKTCDWLPKPNMSASCKRIVDSYLPVILDIIKG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMSRPGEVCSALNICESLQKHLABILNHQKQLESNKIPELDMTEVVAPFMANIPLLLYPQD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 LILLETICGPGTAVWATSPLACAGGPEFWCQSLEQALQCKALGHCLQEVWGHVGADDL-C 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pulmonary surfactant protein B precursor - rabbit N; Alternate names: pulmonary surfactant-associated protein-B C; Species: Oryctolagus cuniculus (domestic rabbit) C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VICKACEYVVKKVMELIDINRTEEKIIHALDSVCALLPESVSEVCQEVVDTYGDSIVALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 261; DB 2;
Pred. No. 1e-10;
18; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 LEEVSPELVCSMLHLC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 LQEMSPELVCSELGLC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.8%;
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Best Local Similarity 61.84
Matches 47; Conservative
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Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Surfactant protein B - rabbit
G.Species: Oryctolagus cuniculus (domestic rabbit)
C.Species: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C.Species: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C.Accession: 146531
A.R. J. Physiol. 268, 1481-1490, 1995
A.Pitle: Transcription and mRNA stability regulate developmental and hormonal expression
A.Reference number: 146531
A.Reference number: 146531
A.Recidue: preliminary; translated from GB/EMBL/DDBJ
A.Recidue: preliminary; translated from GB/EMBL/DDBJ
A.Recidues: 1-369 cMAR>
A.Recidues: 1-369 cMAR>
A.Cooss-references: UNIPROT:PI5285; UNIPARC:UPI000016C51A; EMBL:U17106; NID:g642487; PID
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                                                                                                                                                                                                    472
                                                                                                                                                                                                                                              360 VVDTYGSSILSILLEEVSPELVÇSMLHLCS----GTRLPALTVHVTQPKDGGFCEVCKK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCDICKDVVTAAGDMLKDNATEERILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDII 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 QDGPRSKPQPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADIC 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 KNYISQYSEIAIQMMMHMQPKEICALVGFCDEVKEMPMQTLVPAKVASKNVIPALELVEP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AORFPIPL----P 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 IKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILD-AFDKMCSKLPKSLSEECQEV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AERYTVILLEVLLGHVLPQLVCGLVLRCSSVDSIGQVPPTLEALPGEWLPQDPR-CRLCM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 KLVGYLDRNLEKNSTKQEILAA----LEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVE 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVITQA-RNISEQTRPQAVYHACLSSQLDK-----QECEQEVELHTPQLLSLLSR 340
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                                                   LVGYLDRNLEKNSTKQEILAALEKGC--SFLPDPYQKQCDQFVAEYEPVLIBILVEVMDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 KGEMSRPGEVCSALNLCESLOKHLAELNHOKOLESNKIPELDMTEVVAPFWANIPLLLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YALPLIASLLGAALAGPVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 WLÍLLILPTICGPGTÁVWATSPLACAQGPERWCQSLEQALQCKALGHCLQEVWGHVGADDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Gene: SP-B C, Superfamily: pulmonary surfactant protein B, saposin repeat homology F_161-153/Domain: saposin repeat homology <SAP1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.8%; Score 301.5; DB 2; Best Local Similarity 21.6%; Pred. No. 1.5e-12; Matches 111; Conservative 66; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :| :||| : ||| GWDARAICQALGACVATLSPL----QCIQSPHF 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 VMDPSFVCLKIGACPSAHKPLLGTEKCIWGPSY 501
                                                                                                                                                                                                                                                                                                                                                                                                    501
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTTCQALGACRITFSPL---QCIHIPHF 363
                                                                                                                                                                                                                                                                                                                                                                                                    SFVCLKIGACPSAHKPLLGTEKCIWGPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 166 -GALPAKP------
                                                                                                                                                                                               415
                                                                                                                                                                                                                                                                                                                                                                                          473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292
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C:Accession: T48201
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mewf submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24488
A;Accession: T48201
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residuss: 1-217 <BEV>
A;Residuss: 1-217 <BEV>
A;Residuss: cultivar Columbia; BAC clone T20L15
A;Experimental source: cultivar Columbia; BAC clone T20L15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q18279; UNIPARC:UP10000076C88; EMBL:U40797; NID:g1065916; P
A;Experimental source: strain Bristol N2; clone C28C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 YISQYSEIAIQMMMHM-QPKEICALVGFCDEVKEMPMQTLVFAKVASKNVIPALELVEPI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 KKHEVPAKSDVYCEVCEPLVKEVTKLIDNNKTEKEILDAFDKMCSKLFKSLSEECQEVVD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 ĠAQŚAPSP-----ĊESĊKSMYQNFIDASKDRMKMAQLKVS-LSMLC--VGTSHQSDĊSK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 ÇQEVVPTYGSSILSILLEEVSPELVÇSMLHLÇSGTRLPALTVHYTQPKDGGFÇEVÇKTLY 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 GYLDRNIEKNSTKOBILAALBKGCSFLPDPYQKQCDQFVABYBPVLIBILVBVMDPSFVC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 GPRSKPOPKDNGDVCQDCIQMYTDIQTAVRINSTFVQALVEHVKEECDRLGPGMADICKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 TLDKLDFIÅYKLAPYLADTSAVCSKLOMCGESQFSPLARLAMLYLKKSEAİVÅ---NDNİ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C28C12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 LVEPIKK-HEVPAKSDVYCEVCEPLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 6.3%; Score 176.5; DB 2; Length 402;
1 Similarity 20.3%; Pred. No. 0.00029;
75; Conservative 58; Mismatches 156; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 4
A;Introns: 29/3; 82/3; 124/3; 151/3; 258/3; 318/1; 372/3; 400/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rimiler, N. submitted to the EMBL Data Library, November 1995 submitted to the EMBL Data Library, November 1995 submitted to the sequence of C. elegans cosmid C28C12. A; Description: The sequence of C. elegans cosmid C28C12. A; Accession: T15677 A; Accession: T15677 A; A; Exturbly DBJ A; Malecule type: DNA A; Malecule type: DNA A; Mesidues: 1-402 < MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 7.3%; Score 203.5; DB 2;
1 Similarity 27.8%; Pred. No. 2.2e-06;
52; Conservative 40; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                          A; Map position: 5
A;Introns: 30/1; 79/3; 146/3; 166/3
A;Note: T20L15.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477 LKIGACP 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TILHVCP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: CESP:C28C12.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S:
Matches 75,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T18N14.110 - Arabidopeis thaliana hypothetical protein T18N14.110 - Arabidopeis thaliana ("Gispecies Arabidopeis thaliana ("Gispecies Perb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 C; Accession: T4605 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 K;; Fibelsenty, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.; Stabelsence number: Z23013 A; Reference number: Z23013 A; Accession: T46069 A; Accession: T46069 A; Accession: Treliminary A; Molecule type: DNA A; Residues: 1213 CDELA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 GYSQQCISLVDYY-VPLFFLQLESFQPHYFCKRMNLCG--KVVALVBEARQDS----CGV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKKLYGYLDRNIEKNSTKQEILAALEKGCSFLPDPYQKQCDQFYAEYEPVLIEILVEVMD 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 VIPALELVEPIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 SLSEECQEVVDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEV 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 VGYLDRNLEKNSTKORILAA-----LEKGCSFLPDPYQKQCDOFVAEYEPVLIBILVEVM 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTQA-RNISEQTRPQAVXHACLSSQLDK------QECEQFVAAHAP-----AA 335
                                                                                                                                                                                                                                                                                                                                                                                        363 TYGSSILSILLEBVSPELVCSMLHLCS----GTRLPALTVHVTQ--PKDGGFCEVCKKL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :| :|| | :|| | :|| | 334 | 336 | 337 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 338 | 3
                                                                                                                                                                                                                                                                                          176 -----HTQ-----HTQ----- DDLSAQPPPIPLP--------- 190
                                                                                                                                                                                                                                                                                                                                                       304 KHEVPAKSDVYÇEVÇEPLVKEVTKLIDNNKTEKEILD-AFDKMÇSKLPKSLSEEÇÇEVVD 362
                                                                                                                      GPRSKPOPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADICKN 243
                                                                                                                                                                                175
                                                                                                                                                                                                                                    244 YISQYSBIAIQMMHMQPKBICALVGFCDEVKEMPMQTLVPAKVASKNVIPALBLVEPIK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypotein protein T20115.70 - Arabidopsis thaliana
hypotes: Arabidopsis thaliana (mouse-ear cress)
C;Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                         QINAKA-ICQHLGLCQ-----G 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:09SCT5; UNIPARC:UPI00000AC273; EMBL:AL132968
A;Cross-references: UNIPROT:09SCT5; UNIPARC:UPI00000AC273; EMBL:AL132968
A;Experimental source: cultivar Columbia; BAC clone T18N14
A;Genetics:
A;Map position: 3
A;Introns: 31/1; 80/3; 146/3; 166/3
A;Note: T18N14.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471 DPSFVCLKIGACPSAHKPLLGTE------KCIWGPSY 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.6%; Score 213; DB 2.
Similarity 29.7%; Pred. No. 5e-07;
57; Conservative 35; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.7%
Matches 57; Conservative
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OM protein - protein search, using sw model

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1852.779 Million cell updates/sec
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1852.779 Million cell updates/sec Title: US-10-801-517-1 .
Perfect score: 2789
Sequence: 1 MYALFLLASLLGAALAGPVL......NTETAAQCNAVEHCKRHVMN 524

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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PROTEIN SEQUENCE OF 17-24; 165-172; 180-189 AND 298-302.

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MEDLINE=89000190; PubMed=3048308;
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61 LPCDICKOVVTAAGDMLKDNATBEBILVYLBKTCDWLPKPNNSASCKBIVDSYLPVILDI
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   EMBL; AC073370; CAI40837.1; JOINED; Genomic_DNA.
GO; GO:0005764; C:lygosome; IEA.
GO; GO:0006629; P:lipid metabolism; IEA.
GO; GO:006665; P:sphingolipid metabolism; IEA.
SEQUENCE 524 AA; 58112 MW; 71977PABC9EI533 CRC64;
                                                                                                                                                                                           100.0%; Score 2789; DB 2;
100.0%; Pred. No. 1.3e-173;
ive 0; Mismatches 0;
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TISSUE=Synovial membrane;
Maruyama K., Sugano S.;
                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 524; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q53FJS_HUMAN PRELIMINARY;
Q53FJS;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                     1 MYALFILASLIGAALAGPVIGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS
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Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin
Phelan M., Farmer A.;
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10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31)
Prosaposin (Variant Gaucher disease and variant metachromatic
                                                                                                Length 524;
Amoresano A., Vaccaro A.M.; "Structural and membrane-binding properties of saposin D.";
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EMBL; AL731541; CAI40837.1; -; Genomic_DNA.
EMBL; BT006849; AAP35495.1; -; mRNA.
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                                                                                          Query Match 100.0%; Score 2789; DB 1; Best Local Similarity 100.0%; Pred. No. 1.3e-173; Matches 524; Conservative 0; Mismatches 0;
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Name=PSAP; ORFNames=RP11-472K8.1-001;
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421 RNLEKNSTKQEILAALEKGCSFLPDPYQKQCDQPVABYEPVLIEILVEVMDPSFVCLKIG 480
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
16-SEP-2005 (TrEMBLrel. 31, Last annotation metachromatic
16-SEP-2005 (TrEMBLrel. 31, Last annotation metachromatic
16-SEP-2005 (TrEMBLrel. 31, Last annotation update)
16-SEP-2005 (TrEMBLrel. 31, Last annotation update)
17-SEP-2005 (TrEMBLrel. 31, Created update)
18-SEP-2005 (TrEMBLrel. 31, Created update)
18-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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18-SEP-2005 (TrEMBLRel. 31, Last annotatio
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Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
"Construction and characterization of a full length-enriched and a 5'-
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CA140836.1; JOINED; Genomic_DNA
         EMBL; AC073370;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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OSJOAT HUMAN PRELIMINARY; PRT; 559 AA.
10-MAY-2005 (TYEMBLrel. 30, Last sequence update)
10-MAY-2005 (TYEMBLrel. 30, Last annotation update)
Progaposin (Variant Gaucher disease and variant metachromatic
                                                                                                                                                                                                                                                                  ö
                                                                      NUCLEOTIDE SEQUENCE.
TISSUE-Synovial membrane;
TISSUE-Synovial membrane;
Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki
Tanaka A., Yokoyama S.,
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AK223290; BAD97010.1; -; mRNA.
                                                                                                                                                                                                                            Query Match

99.9%; Score 2785; DB 2; Length 524;
Best Local Similarity 99.8%; Pred. No. 2.3e-173;
Matches 523; Conservative 1; Mismatches 0; Indels
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL731541; CAI40836.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       524 AA; 58140 MW; 7034F0C71C2226BC CRC64;
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Name-PSAP; ORFNames-RP11-472K8.1-002;
Homo sapiens (Human).
                       end-enriched cDNA library.";
Gene 200:149-156(1997).
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Prosaposin variant (Fragment).
Name-prosaposin variant;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 IKGEMSRPGEVCSALNLCESLOKHLAELNHQKQLESNKIPELDMTEVVAPFMANIPLLLY
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                                                                                                                                                                                                                                                                                                                                       Query Match
99.8%; Score 2783; DB 2; L
Best Local Similarity 100.0%; Pred. No. 3.4e-173;
Matches 523; Conservative 0; Mismatches 0;
EMBL; AUC/33/0; CAITAUSSO: I. COLINEL; AUC/33/0; CAITAUSSO: SMR; QSJQ37; 194-272, 311-390.

SMR; QSJQ037; 194-272, 311-390.

GO; GO:0006659; P:11pid metabolism; IEA.

GO; GO:0006656; P:ppinigolipid metabolism; IEA.

InterPro; IPRO03119; SapA.

InterPro; IPRO08149; SapB 1.

InterPro; IPRO08139; SapOsinB.

InterPro; IPRO08139; SapOsinB.

InterPro; IPRO08139; SapOsinB.

Pfam; PFO2199; SapB 1; 4.

Pfam; PFO3189; SapB 2; 4.

PRINTS; RRO1797; SapB Sub; 2.

SMART; SMO0122; SapB Sub; 2.

SMART; SMO0122; SapB Sub; 2.

SMART; SMO0132; SapB Sub; 2.
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Q59ENS HUMAN PRELIMINARY;
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IKGEMSRPGEVCSALNLCESIQKHLAELNHQKQLESNKIPELDMTEVVAPFMANIPLLLY 180
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QSR4U7
QSR4U7
01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp459J1314.
Name=DKFZp459J1314;
Pongo pygmaeus (Orangutan).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 527;
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to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 527 AA; 58469 MW; 293FBB746C29C4D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
            EMBL; CR026102; CAI29728.1; EMBA.

SMR; QSNVD5; 194-275, 314-393.

GO; GO:0006629; P:11pid metabolism; IEA.

GO; GO:0006629; P:1pid metabolism; IEA.

GO; GO:0006629; P:1pid metabolism; IEA.

GO; GO:0006629; P:1pid metabolism; IEA.

INTERPO; IPRO01819; SapA.

INTERPO; IPRO08118; SapB 2.

INTERPO; IPRO0819; SapB 2.

INTERPO; IPRO0819; SapOsin.

INTERPO; IPRO0819; SapOsin.

Pfam; PPO2199; SapA; 2.

Pfam; PPO2199; SapB 1; 4.

Pfam; PPO3184; SapB 1; 4.

Pfam; PPO3184; SapB 2; 4.

ProDom; PDO3173; SapOsIN.

ProDom; PD001732; SapB 3b; 2.

PRODOM; SAPA; 2.

SWRRT; SM0162; SAPA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 8.3e-173;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.6%; Score 2776.5; 99.2%; Pred. No. 8.3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.2
Matches 523; Conservative
  (NOV-2004)
  Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 YLDRNILEKNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCL 483
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 QEVVDIYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKGUVG
                                                                                                                                                                                                                                                                                                                                                                                       124 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKQLESNKIPBLDMTEVVAPFMANIPLLLY
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                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                           Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S. Ohara O., Nagase T., Kikuno F.R.; "None Title."; Toyods T., Kikuno F.R.; Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                       Query Match
99.6%; Score 2777.5; DB 2; Length 530;
Best Local Similarity 99.4%; Pred. No. 7.2e-173;
Matches 524; Conservative 0; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIGACPSAHKPLLGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN 524
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                                                                                                                                                                                                                                         530 AA; 58727 MW; 6CA1F0159B182BC9 CRC64;
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QSNVDS;
QSNVDS;
01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
Hypothetical protein DKFZp459F0110.
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Wambutt R., Heubner D., Mewes H.W., Weil B., Amid
Pobo G., Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pongo pygmaeus (Orangutan)
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TISSUE=Cortex;
                                                NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=9600;
  NCBI_TaxID=9606;
                                                                                                                                                                                                                     NON TER
SEQUENCE
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Q4R590_MACFA PRELIMINARY;
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NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LPCDICKDVVTAAGDMLKDNATEEEILVYLEKTCDWLPKPNWSASCKEIVDSYLPVILDI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVVAPFMANIPLLLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                               MYALFLLASLLGAALAGPVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPCDICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI
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                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                Length 526;
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                                                                                      Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B. Osanger A., Fobo G., Han M., Wiemann S.; Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                       CF3B146DDB6F5539 CRC64;
                                                                                                                                                   GO; GO: 0005764; C: 1ysosome; IEA.
GO; GO: 0006629; P: 1hpid metabolism; IEA.
GO; GO: 0006665; P: sphingolipid metabolism; IEA.
InterPro; IPR003119; Saph.
InterPro; IPR008136; Saph.
InterPro; IPR008136; Saph.
InterPro; IPR008139; Saph.
InterPro; IPR008139; Saposin.
InterPro; IPR008139; Saposin.
Pfam; PP05184; Saph.; 2.
Pfam; PP05184; Saph.; 2.
Pfam; PP05184; Saph.; 2.
Probom; SM0162; Saph.; 2.
SMART; SM01062; SAPA; 2.
                                                                                                                                                                                                                                                                                                                                                                            Score 2770; DB 2;
Pred. No. 2.2e-172;
1; Mismatches 1;
                                                                                                                              CR861144; CAH93219.1; -; mRNA. QSR4U7; 194-274, 313-392.
                                                                                                                                                                                                                                                                                                                                              1 protein.
526 AA; 58325 MW;
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.2%;
Matches 522; Conservative
                                                                              German cDNA Consortium;
                                                      NUCLEOTIDE SEQUENCE
                     Pongo.
NCBI_TaxID=9600;
       mmalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MYALFLIASILGAALAGPVIGIKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS
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           13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-Brain cDNA, clone: QccE-13090, similar to human prosaposin (variant Gaucher disease and variantmetachromatic leukodystrophy) (PSAP), (Brain cDNA, clone: QccE-13989, similar to human prosaposin (variant Gaucher disease and variantmetachromatic leukodystrophy)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           International consortium for macaque cDNA sequencing, analysis; "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications."; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WCLEOTIDE SEQUENCE.
Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
"Substitution rate and structural divergence of 5'UTR evolution:
Comparative analysis between human and cynomolgus monkey cDNAs.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB169557; BAE01735.1; -; mRNA.
EMBL; AB169527; BAE01069.1; -; mRNA.
SEQUENCE 497 AA; 55306 MW; 4A1974FBDB883900 CRC64;
                                                                                                                                                                                                                                                                 Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
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97.9%; Pred. No. 1.3e-151;
ative 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                       TaxID=9541;
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P26779; Q9N2G4;
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SAP_BOVIN
ID SAP_BC
AC P26775
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LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
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                  R Pfam; PF05184; SapB_1; 4.

R Pfam; PF05188; SapB_1; 4.

PRINTS; PR01499; SapB_2; 4.

R PRINTS; PR01799; SapB_2in.

R Probom; PD001732; SapB_sub; 2.

R Probom; PD001732; SapB_sub; 2.

R PROSTT; SM00162; SaPA; 2.

R PROSTTE; PS50115; SapB_3; 2.

R PROSTTE; PS50115; SapB_3; 3.

M Repeat; Signal; Sphingolipid metabolism; Lysosome; 3.

T GNAL 1 16 Potential.

T CHAIN 60 142 Saposin A.

T CHAIN 196 275 Saposin B.

T CHAIN 196 275 Saposin B.

T CHAIN 196 275 Saposin B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
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.) (Potential)
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84.2%; Pred. No. 6.7e-150;
tive 45; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B -> Q (in Ref. 2).
R -> S (in Ref. 1).
293AFC0FB9C4FA99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Saposin A-type 1.
Saposin B-type 1.
Saposin B-type 2.
Saposin B-type 3.
Saposin B-type 4.
Saposin A-type 2.
N-linked (GlCNAC.)
N-linked (GlCNAC.)
N-linked (GlCNAC.)
N-linked (GlCNAC.)
N-linked (GlCNAC.)
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nes 442; Conservative
      Pfam; PF02199; SapA; 2.
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441
127
260
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525 AA;
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01-AUG-1992 (Rel. 23, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Saposin B (Sphingolipid activator protein 1) (SAP-1) (Gerebroside sulfate activator) (CSACt) (Dispersin) (Sulfatide/GM1 activator);
Saposin C (Co-beta-glucosidase) (Al activator) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D
(Protein C) (Component C)].
                                                                                                                                                                                  Bos taurus (Bovine).

Bukaryota, Metasota, Chordata, Craniata, Vertebrata, Buteleostomi;

Mammalia, Butheria, Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                          [1] —
NUCLECTIDE SEQUENCE, AND VARIANTS.
NUCLECTIDE SEQUENCE, AND VARIANTS.
TISSUE-Mammary gland;
Azua N., Yoshide K.;
"RT-PCR cloning of bovine prosaposin.";
"RT-PCR cloning of bovine prosaposin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro, IPR009007; Pept_Aspartc_cat.
InterPro, IPR003119; SapA.
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Surfactant_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IPR007856; Sapa 1.
7 IPR008139; Sapa 2.
7 IPR008140; Sapa sub.
7 IPR008373; SaposinB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 312-391
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InterPro;
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312
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                                                                       MAHM---QPKEICALVGFCDEVKEMPMQTLVPAKVASKNVIPALELVEPIKKHEVPAKSD
                                                                                                     LEBVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGPCEVCKKLVGYLDRNLEKNSTKQET
                                                                                                                                                                                                                                                                                            LAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIGACPSAHKPLLGT
                                                                                                                                                                                                                                                                                                                                                                                  P10560; Q62841; Q64190; O1-JUL-1989 (Rel. 11, Created) O1-JUL-1989 (Rel. 11, Created) O1-JUL-1989 (Rel. 11, Last sequence update) O1-JUL-1989 (Rel. 11, Last annotation update) Sulfated glycoprotein 1 precursor (SGP-1) (Prosaposin). Name-Psap; Synonyms-Sgpl; Rattus norvegicus (Rat). Bukaryota; Metazos; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buzchontoglires; Glires; Rodentia; Sciurognathi; Muroides; Muridae; Murinae; Rattus.
                                                                                                                                                                       VYCEVCEFLUKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSILSIL
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MEDINE-8900647; PubMed=3048385;
MEDINE-8900647; PubMed=3048385;
COllard M.W., Sylvester S.R., Teuruta J.K., Griswold M.D.;
"Biosynthesis and molecular cloning of sulfated glycoprotein secreted by rat Sertoli cells: sequence similarity with the 7 secreted by rat Sertoli cells: sequence similarity with the 7 silodalton precursor to sulfatide/GM1 activator.";
Biochemistry 27:4557-4564(1988).
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NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE
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J. High SUBCELLULAR LOCATION: Extracellular.
-!- SUBILARITY: Contains 2 saposin A-type domains.
-!- SIMILARITY: Contains 4 saposin B-type domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            BKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN 524
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NUCLEOTIDE SEQUENCE [MRNA].
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                   MCKNYINQYSEVAIQMVMHMQPKEICVLAGPCDEVKEMPMKTLVPAEVVSENVIPALGLV 300
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                        WYDTYGSSILSILLEBVSPELVCSMIHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYL
                                                                                                                                                                                      BPIKKHEVPAKSDVYCEVCEPLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSBECQE
                                                                                                                                                                                                                                                         DRNLEKNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKI
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                                                                                                                                                                                                                                                                                                                                                    GACPSAHKPLLGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN 524
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99.1%; Pred. No. 1.2e-146;
tive 1; Mismatches 0;
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Interpro; IPR003139; SapB 2.
Interpro; IPR008139; SapB 3.
Interpro; IPR008139; SapB 3.
Interpro; IPR008139; SapOsinB.
PEam; PP02199; SapB 1; 4.
PEam; PP02199; SapB 1; 4.
PEam; PP03189; SapB 1; 4.
PEAM; PR05184; SapB 1; 4.
PEDD: PR05184; SapB 1; 4.
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SEQUENCE 452 AA; 50664 MW;
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Matches 448; Conservative
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NCBI_TaxID=9600;
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TISSUB-Prostate.

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A Straubberg R.L., Feingold B.A., Groube L.H., Derge J.G.,

A Straubberg R.L., Feingold B.A., Groube L.H., Derge J.G.,

A Lauberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Lachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

D Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramoon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahe, J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

C Generation and initial analysis of more than 15,000 full-length human
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180 PQDRPRSQPQPKANEDVCQDCMKLVTDIQTAVRTNSSFVQGLVDHVKBDCDRLGPGVSDI 239
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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Last annotation update)
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> B (in Ref. 2).
> V (in Ref. 3).
> R (in Ref. 3).
> M (in Ref. 3).
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Saposin B-type 1.
Saposin B-type 2.
Saposin B-type 3.
Saposin B-type 4.
Saposin B-type 4.
Saposin B-type 4.
Saposin B-type 4.
N-linked (GlCNAC...) (N-linked (
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                                                                                                                                                                                                                                  GO, 5046936; P:91ycolipid transport; NAS.
InterPro; IPR003007; Pept_Aspartc_cat.
InterPro; IPR003119; SapA.
InterPro; IPR003119; SapB.
InterPro; IPR008138; SapB.
InterPro; IPR008138; SapB.
InterPro; IPR008139; SapOsinB.
InterPro; IPR008139; SapOsinB.
InterPro; IPR008139; SapOsinB.
Pfam; PP05199; SapA; 2.
Pfam; PP05184; SapB. 1; 3.
Pfam; PP05189; SapB. 2; 4.
PRINTS; PR01797; SAPOSIN.
PRODOM; PD001732; SapB. 8ub; 1.
PROSITE; PS50110; SAP A; 2.
PROSITE; PS50110; SAP B; 4.
                                                                                                                        HSSP, Q92739; 1N69.
SMR; P10960; 195-271.
Ensembl; ENSRNGG00000000571; Rattus norvegicus.
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mRNA.
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   EMBL; M19936; AAA42136.1;
EMBL; S81353; AAB36042.2;
EMBL; S81373; AAB36233.2;
PIR; A28716; A28716.
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554 AA;
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Matches 368; Conserv
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456
456
63
66
197
229
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                          1 MYALFILASILGAALAGPVLGIKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS
                                                                                                                                                                                           61 LPCDICKDVVTAAGDMLKDNATEREILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI
                                                                                                                                                                                                                                                       121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVVAPFMANIPLLLY
                                                                                                                                                                                                                                                                                          PODGPRSKPOPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEBCDRLGPGMADI
                                                                                                                                                                Gapa
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
MUS musculus 2 days neonate thymus thymic cells CDNA, RIKEN full-
length enriched library, clone:8430014812 product:prosaposin, full
insert sequence (Mus musculus kidney CCL-142 RAG CDNA, RIKEN full
length enriched library, clone:6430050607 product:prosaposin, full
                                                                                                                                                                33;
                                                                                                                                                DB 2; Length 553;
                                                                                                                                              71.1%; Score 1982.5; DB 2; Length 66.3%; Pred. No. 5.7e-121; ive 75; Mismatches 79; Indele
                                                                                                                             553 AA; 61039 MW; 63F3DD5E0C523393 CRC64;
          metabolism; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              554 AA.
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 GO:0006629; P:lipid metabolism;
GO:0006665; P:sphingolipid metab
                InterPro; IPR003119; SapA.
InterPro; IPR003119; SapB.1.
InterPro; IPR001818; SapB.1.
InterPro; IPR008139; SapB.2.
InterPro; IPR008139; SapOsin.
InterPro; IPR008139; SapOsin.
Pfam; PP02199; SapA. 2.
Pfam; PP05199; SapB.1; 3.
Pfam; PP03489; SapB.2; 4.
PRINTS; PR01797; SAPOSIN.
PRODOM; PP001732; SAPB. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          510 AQCNAVEHCKRHVWN 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBBPQ1 MOUSE PRELIMINARY;
QBBPQ1;
                                                                                                                                               Query Match
Best Local Similarity 66.3
Matches 368; Conservative
                                                                                                                     SMART; SM00162; SAPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insert sequence) .
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NUCLECTIONS SEQUENCE.

REATINATIONS and BALBAC. TISSUE-Kidney, and Thymus;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishil Y.,

RA Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S.,

Arakawa T., Sato M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Isawa M., Nishi K., Giosi C., King B., Kochiwa H.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Aizawa K., Isawa M., Nishi K., Gissi C., King B., Kochiwa H.,

RA Saito T., Okaserland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Balake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Balake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Barchiselm M.J., Bult C., Rletcher C., Fujita M., Gariboldi M.,

B., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,

R., Narokone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

R., Saaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

R., Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

R., Wansehlashi V.,
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REATINHOD, and BALB/C; TISSUE=Thymus, and Kidney;

REATINHOD, and BALB/C; TISSUE=Thymus, and Kidney;

RA OKAZAKI Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suruki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suruki H., Schonbach C., Gojobori T.,

RA Andarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,

RA Schriml L.M., Kanapin A., Mateuda H., Datla E., Cousins S.,

RA Schriml L.M., Kanapin A., Hirokawa N., Jackson I.S., Cousins S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Achai A., Kawaji H., Kawasawa Y., Kedzierski R.M., Kings B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Madlott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nogashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Red D.J., Reid J., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,

RA Sultana R., Wannaka Y., Taylor M.S., Taeadale R.D., Tomita M.,

RA Warane-Kishikawa T., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hara A., Hashitume W., Innotani K., Ishii Y., Itoh M., Kagawa I.,

RA Hara A., Hashitume W., Imotani K., Ishii Y., Sinhagawa R.,

RA Hirozane-Kishikawa T., Sasaki D., Shibata K., Shinagawa R.,

RA Hira R., Hashitume W., Imotani K., Lander E.S., Rogers J.,

RA Hara A., Hashitume W., Imotani K., Lander E.S., Rogers J.,

RA Hara A., Hashitume W., Sasaki D., Shibata K., Shinagawa R.,

Ra Birney R. Haysahizaki Y.,

RA Hara A., Hashitume W., Satoki K.,

RA Hara A., Hashitume W., Satoki K.,

RA Birney R. A., Schall C., Seasaki D., Shibata K., Shinagawa I.,

RA Hara A., Ha
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE.
STRAIN-NOD, and BALB/C; TISSUE-Kidney, and Thymus;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=NOD, and BALB/C; TISSUE=Kidney, and Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meth. Enzymol. 303:19-44(1999).
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                                                                                                                           Muridae; Murinae; Mus.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                             NCBI_TaxID=10090;
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This Swiss-Prot entry is copyright. It is produced through a collaboration
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                                                                                                                                                 CKNYISQYSEIAIQMMHMQPKEICALVGFCDEVKEMPMQTLVPAKVASKNVIPALELVE
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                                                                                                                                                                                                                           301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEV
                                                                                                                                                                                                                                                                                                                                       361 VDTYGSSILSILLEEVSPELVCSMLHLCSG-----------
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sclurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94272317; PubMed-8003952; Sprecher-Levy H., Orr-Urtreger A., Lonai P., Horowitz M.; Murine prosaposin: expression in the reproductive system of a implicated in human genetic disease."; Cell. Mol. Biol. 40:233-233(1994).
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MEDIINE=96084310; PubMed=8565332;
Cao Q.P., Crain W.R.;
"Expression of SGP-1 mRNA in preimplantation mouse embryos.";
Dev. Genet. 17:263-271(1995).
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STRAIN=BALB/c; TISSUE=Liver;
Zhao Q.Q., Hay N.N., Morales C.R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAP MOUSE STANDARD; PRT; 557 AA. 601207; Q60861; Q64006; Q64219; L5-DEC-1998 (Rel. 37, Created) L5-DEC-1998 (Rel. 37, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) Sulfaced glycoprotein 1 precursor (SGP-1) (Prosaposin) Names-Bap; Synonyma=Sgpl; Mus musculus (Mouse).
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"The primary structure of mouse saposin.";
Biochem. Biophys. Res. Commun. 184:1266-1272(1992).
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-i- SIMILARITY: Contains 2 saposin A-type domains.
-i- SIMILARITY: Contains 4 saposin B-type domains.
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MEDLINE=92272718; PubMed=1590788;
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RA Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Ra Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Para Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Para P., Hara A., Habilzune W., Harozane T., Hara A., Habilzune W., Harozane T., Hara A., Habilzune W., Harozane T., Hara A., Habilzune W., Sancha H., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Rodawa T., Yakamara M., Nakamura M., Nakamura T., Miyazaki A., Murata M., Nakamura Y., Namura K., Numazaki R., Ohno M., Ohaato N., Okazaki Y., Saitoh H., Sakai C., Sakazume N., Sanc H., Sakai C., Sakazume N., Sanc H., Sakai C., Sakazume N., Sanc H., Satoh H., Sakai C., Sakazume N., Sanc H., Tagama T., Yagawa A., Zikhahashi P., Takaku-Akahira S., Takeda Y., Tanaka T., R. Tomaru A., Toya T., Yasumishi A., Muramatu M., Hayashizaki Y.; DR Tomaru A., Toya T., Yasumishi A., Muramatu M., Hayashizaki Y.; DR EMBL, AKO693698 BAC41036.1; -; mRNA.

Rabi Aki Qabedi I.55-271.

DR RASP, Qapedi S., Sapaba I.

R KIRI S., MGI 197783; Papp.

R KGJ GO:00054739; C:aktrochudrion; IDA.

R InterPro; IPR008130; Sapaba I.

R Fam; PP03489; Sapaba I.

R SAMRT; SM00162; SAPAi I.

R SAMRT; SM00162; SAPAi I.

R SAMRT; SM00162; SAPAi I.

R SAMRT; SM00162; SAPAi I.

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                   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y., Nuramatsu M., Hayashizaki Y., Nuramatsu M., Hayashizaki Y., prepare inli-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                          MEDLINE-205. And BALB/C; TISSUE-Kidney, and Thymus; MEDLINE-2050913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Medline T., Atkiyama J., Mishi K., Nagaoka Y., Tashiro H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshikayi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okasaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Riken integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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64.0%; Pred. No. 7.6e-119;
ive 78; Mismatches 90;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Proactivator polypeptide precursor (Contains: Saposin A; Saposin B;
Saposin C; Saposin D].
Saposin C; Saposin D].
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Phasianidae; Phasianinae;
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TISSUE-Brain, and Liver;
MEDLINE-98129745; PubMed-9461526;
Azuma N., Seo H.-C., Lie O., Fu Q., Gould R.M., Hiraiwa M., Burt |
Paton I.R., Morrice D.R., O'Brien J.S., Kishimoto Y.;
Paton I.R., Morrice D.R., O'Brien J.S., Kishimoto Y.;
Blochem. J. 330:321-327(1998).
                                                                    Gaps
                                           69.5%; Score 1938.5; DB 1; Length 557; 63.6%; Pred. No. 4.3e-118; ative 78; Mismatches 90; Indels 35;
445 445 C -> F (in Ref. 3).
448 448 L -> P (in Ref. 4).
557 AA; 61422 MW; 1345935204995355 CRC64;
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EMBL; 027340; AAB32567.1; "RENA.
EMBL; 027399; 105799; "AB002695.1; "Genomic_DNA.
PIR; JH0604; JH0604.
HSBP; Q92739; 1N69.
SMR; Q61207; 195-274.
EMBENDI; ENSWUSG0000004207; Mus musculus.
ENSWR; Q61207; 195-274.
ENSWR; Q61207; 195-274.
ENSWR; Q61207; 195-274.
ENSWR; Q61207; 195-274.
ENTERPO: PRO0913; Cextracellular space; TAS.
GO; GO:0005713; Cextracellular space; TAS.
ENTERPO: PRO0913; SapA.
INTERPO: PRO0913; SapB.
ENTERPO: PRO0913; SapOsin.
R InterPo: PRO0913; SapOsin.
R InterPo: PRO0913; SapOsin.
R Pfam; PF02199; SapA; 2.
R Pfam; PF02199; SapA; 2.
R Pfam; PF02199; SapA; 2.
R Pfam; PF03184; SapB. 2; 4.
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PRODOM; PRO01732; SAPOSIN.
PROSITE; PS51110; SAP A: 2.
PROSITE; PS5015; SAP B; 4.
Glycoprotein; Repeat; Signal.
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Lubraticed (NOV-1998) to the EMBL/GenBank/DDBJ databases.

Lubraticed (NOV-1998) to the EMBL/GenBank/DDBJ databases.

C -1- FUNCTION: The lysosomal degradation of sphingolipids takes place by the sequential action of specific hydrolases. Some of these enzymes require specific low-molecular mass, non-enzymic proteins: the sphingolipids activator proteins (coproteins) (By similarity).

CC -1- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of galactosylceramide by beta-galactosylceramidase (EC 3.2.1.4.5) and galactosylceramide by beta-galactosylceramidase (EC 3.2.1.4.6).

Saposin C apparently acts by combining with the enzyme and acidic lipid to form an activated complex, rather than by solubilizing the substrate (By similarity).

CC -1- FUNCTION: Saposin B stimulates the hydrolysis of galactocerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1

Gangliosides by beta-galactosidase (EC 3.2.1.22).

CC -1- FUNCTION: Saposin B stimulates the hydrolysis of galactocerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1

Gangliosides by beta-galactosidase A (EC 3.2.1.22).

CC -1- FUNCTION: Saposin B stimularity).

CC -1- FUNCTION: Saposin B is a homodime: (By similarity).

CC -1- FUNCTION: Saposin B is a homodime: (By similarity).

CC -1- FUNCTION: Saposin B is a specific sphingomyelin phosphodiesterase activator (EC 3.1.4.12) (By similarity).

CC -1- FUNCTION: Saposin B is a homodime: (By similarity).

CC -1- FUNCTION: Saposin B is a specific sphingomyelin phosphodiesterase by beta-galactosides (By similarity).

CC -1- FUNCTION: Saposin B is a specific sphingomyelin phosphodiesterase cc amilar to each other and are sphingolipid hydrolase activator proteins (By similarity).

CC -1- FUNCTION: Saposin B is a specific sphingomyelin beta-galactosides which are similar to each other and are sphingolipid for hydrolase activator proteins (By similarity).

CC -1- FUNCTION: Saposin B is a specific sphingomyelin bydrolase activator proteins (By similarity).

CC -1- 
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Matches 301; Conservative
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Search completed: January 13, 2006, 16:34:21 Job time : 202.536 secs



Sequence Sequence Sequence Sequence

Sequence Sequence 1 Sequence 1 Sequence 3

Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 3 Sequence 3

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Pacente 1, Application US/09352548

Pacent No. 6500431

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gill, Parkash S.
TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
TITLE REPERENCE: 017986-000410012
FILE REPERENCE: 017986-00041001
GURRENT APPLICATION NUMBER: US/09/352,548
GURRENT FILING DATE: 1999-07-12
FARLIER APPLICATION NUMBER: US 60/092,647
SARLIER PILING DATE: 1998-07-13
NUMBER OF EQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
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100.0%; Pred. No. 9.8e-243;
ive 0; Mismatches 0;
US-08-584-671-16
US-09-024-192-16
US-09-034-192-16
US-08-584-671-14
US-09-027-376-14
US-09-027-376-14
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US-09-380-380-3
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NAME/KEY: PREFIDE
LOCATION: (195)..(275)
CTHER INFORMATION: Saposin B
US-09-352-548-1
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Best Local Similarity 100.
Matches 524; Conservative
   TYPE: PRT
ORGANISM: Homo sapiens
   RESULT 1
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sequence 23, Appl
sequence 2, Appli
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 3, Appli
Sequence 24, Appli
                                                                                                              January 13, 2006, 16:26:00; Search time 54.6556 Seconds (without alignments) 792.637 Million cell updates/sec
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Sequence
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2789
1 MYALFLIASILGAALAGPVL......NTETAAQCNAVEHCKRHVWN
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/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Length 524; Indels

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181 PQDGPRSKPQPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
361 VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYLD
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INFORMATION FOR SEQ ID NO: 23:
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Best Local Similarity 100.
Matches 524; Conservative
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US-08-928-074-23
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Sequence 6272, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/231,768

PRIOR FLING DATE: 2000-10-20

PRIOR FLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR FLING DATE: 2000-10-03

SOFTWARE: PRESENCE PRESENCE: ERESENCE: SOFTWARE: PRESENCE: ENGLANCE: MINGOWS VETSION 4.0

SOFTWARE: PRESENCE: MINGOWS VETSION 4.0

SEQ ID NO 6272
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                         PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEV
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                                                                                                  VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGF
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100.0%; Pred. No. 9.8e-243;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 524; Conservative
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ORGANISM: Human
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                                               480
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                            421 RNLEKNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG
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IS-08-928-074-23

IS-08-928-074-23

Patent No. 6899602

GRNERAL INFORMATION:

APPLICANT: 0° Brien, John S.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 24

CORRESPONDENCES: 24

COUNTY: 1a Johla

STREET: 4225 Executive Square, Suite 1400

CITY: 1a Johla

STATE: CA

COUNTY: US

ZIP: 92037

COMPUTER: Diskette

COMPUTER: Diskette

COMPUTER: Diskette

COMPUTER: 1EM Compatible

COMPUTER: 1EM Compatible

COMPUTER: 11 FORM:

MEDIUM TYPE: 05-0848: Windows95

SOFTWARE: Patis Windows95

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/611,307

FILING DATE: 05-MAR.1996

PRIOR APPLICATION DATA: PCT/US97/04143

FILING DATE: 05-MAR.1996

PRIOR APPLICATION NUMBER: 205-MAR.1996

PRIOR APPLICATION NUMBER: 08/611,307

APPLICATION NUMBER: PCT/US97/04143

FILING DATE: PLOS-MAR.1996

ATTORNEY AGENT INFORMATION:

NAME: Haile, Ph.D. Lisa A.

RESTERRICE/DOCKET NUMBER: 07256/024001

TELEBOUNDING CALLOR NUMBER: 07256/024001

TELEBOUNDING: 619/678-5070
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100.0%; Pred. No. 9.8e-243;
ive 0; Mismatches 0;
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61 LPCDICKDVVTAAGDMLKDNATEEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
                                                                                                        RNLEKNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
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                                                                                  VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGPCEVCKKLVGYLD
301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEV
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Pred. No. 1e-240;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                     ACPSAHKPLLGTEKCIWGPSYWCONTETAAQCNAVEHCKRHVWN 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: O'BRIEN, JOHN S.
APPLICANT: KISHIMOTO, YASUO
TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITY: NEWPORT BEACH
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92560
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,247
FILING DATE: 19930730
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Nod A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 0BRIEN.002A
TELEPPAK: 619-235-6550
TELEPPAK: 619-235-6156
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US-08-100-247-2
Sequence 2, Application US/08100247
Sequence 100. 5571787
GENERAL INFORMATION:
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Best Local Similarity 99.4%;
Matches 521; Conservative
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TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 amino acid
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CLONE: PROSAPOSIN
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR PAPLICATION NUMBER: 60/231,768

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTHWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8633

LENGTH: 535
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                                                                                      241 CKNYISQYSEIAIQMMAHMQPKEICALVGFCDEVKEMPMQTLVPAKVASKNVIPALELVE 300
                                                                                                                                                 301 PIKKHEVPAKSDVYCEVCEFLVKBVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEV 360
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PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEV
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                                                                                                                                                                                                                                                                                                                                                                                                         481 ACPSAHKPLLGTEKCIWGPSYWCONTETAAQCNAVEHCKRHVWN 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 524; Conservative
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US-09-949-016-8603
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US-09-949-016-8603
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US-08-232-513A-3
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                                                                                                                        PODGPRSKPOPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRIGPGMADI 240
                                                                                                                                                                                                                                                                       CKONYISQYSBIALQMAMHMQPKBICALVGFCDEVKEMPMQTLVPAKVASKNVIPALBLVB 300
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19:-08-756-031-2
5 Sequence 2, Application US/08756031
5 Patent No. 6590074
5 GENERAL INFORMATION:
7 APPLICANT:
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9 APPLICANT:
1 TITLE OF INVENTION:
9 CORRESPONDENCE ADDRESS:
9 CORRESPONDENCE ADDRESS:
9 STREET:
1 CORRESPONDENCE ADDRESS:
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2 CORRESPONDENCE ADDRESS:
3 STREET:
4 COUNTRY:
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ZIP: 9260C
COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
CORTANARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,031
FILING DATE: 26-NOV-1996
CLASSIFICATION NUMBER: 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGRNT INPORMATION:
NAME: ISTAELSEN NUMBER: 29,655
REFERENCY DOCKET NUMBER: 29,655
REFERENCY DOCKET NUMBER: 29,655
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Sequence 3. Application US/08232513A
Batent No. 5700909
GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
TITLE OF INVENTION: as Therapeutic Agents
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                  DB 2; Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 ACPSAHKPLLGTEKCIWGPSYWCONTETAAQCNAVEHCKRHVWN 524
                                                                                                                Score 2766.5; DB 2; Length
Pred. No. 1e-240;
2; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,513A
FILING DATE: 21-APR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Sulte 700
GITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                    Query Match 99.2%;
Best Local Similarity 99.4%;
Matches 521; Conservative
    FRAGMENT TYPE: N-terminal IMMEDIATE SOURCE:
                                                             PROSAPOSIN
ANTI-SENSE: NO
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61 LPCDICKDVVTAAGDMLKDNATEEEILVYLEKTCDMLPKPNMSASCKEIVDSYLPVILDI 120
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Pred. No. 6.7e-240;
                                                                                                                                                      COUNTY OF USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
COMPUTER: TRM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,146A
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/483,146A
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: SPILON OF TRIBORMATION:
NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: MYELOS:002DV1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear STREET: 620 Newport Center Blvd. 16th Floc CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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TYPE: amino acid
STRANDEDNESS: single
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       NUMBER OF SEQUENCES: 11
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Best Local Similarity
                                                                                                                                              USA
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                                                                                                                      STATE: C
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Patent No. 5696080
GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
APPLICANT: Kishimoto, Yasuo
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: THEREFROM
TITLE OF INVENTION: THEREFROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 CKNYISQYSEIAIQMMMHMQPKEICALVGFCDEVKEMPMQTLVPAKVASKAVIPALDLVD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 PIKKHEVPAKSDVYCEVCEPLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEECQEV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYLD 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 RNLEKNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 RNLEKNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LPCDICKDVVTAAGDMLKDNATEEBILVYLGKTCDWLPKPNWSASCKBIVDSYLPVILDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 IKGEMSRPGEVCSALNLCESLOKHLAELNHOKOLESNKIPELDMTEVVAPFMANIPLLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQDGPRSKPQPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKERCDRLGPGMADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 PODGPRSKPOPKD-GDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKBILDAFDKMCSKLPKSLSEEQGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MYALFILLASILGAALAGPVLGLKBCTRGSAVWCQNVKTASDCGAVRHCLQTVWNKPTVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.9%; Score 2759.5; DB 1; Length 523; Best Local Similarity 99.2%; Pred. No. 4.5e-240; Matches 520; Conservative 2; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN 524
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                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
1.00ATION: 1..523
9 OTHER INFORMATION: /label= Hum_prosaposin
US-08-232-513A-3
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/100,247

FILING DATE: 30-JUL-1993

ATTORNEY AGENT INPORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERRICE/POCKET NUMBER: 9-UD 1643

TELEPHONE: (619) 535-9901

TELEPHONE: (619) 535-9901

TELEPK: (619) 535-8949

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 523 amino acids

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-483-146A-2
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GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
APPLICANT: O'Brien, John S.
APPLICANT: Kiehimoco, Yasuo, Y
                                   421 RNLEKNSTKORILAALEKGCSFLPDPYQKQCDQFVAEYBPVLIEILVEVMDPSFVCLKIG 480
                                                                                                                                                                                                                                                                                                                                                                                                           241 CKNYISOYSEIAIOMMHMOPKEICALVGFCDEVKEMPMQTLVPAKVASKNVIPALELVE
                                                                                                                          301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKBILDAFDKMCSKLPKSLSEECQEV
                                                                                                                                                          361 VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 ACPSAHKPLIGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSER: Knobbe, Martens, Olson and Bear STREET: 620 Newport Center Blvd. 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PRELEGE for Windows Version 2.0
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION NUMBER: 08/958.970
FILING DATE: 28-OCT-97
PRIOR APPLICATION NUMBER: 08/483.146
FILING DATE: 07-UUN-1995
APPLICATION NUMBER: 08/100,247
FILING DATE: 30-UUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israeleen, Ned A
REGISTRATION NUMBER: 29,655
REBERENCE/DOCKET NUMBER: MYELOS.2DVICZ
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
108-09-076-258A-2
; Sequence 2, Application US/09076258A
; Patent No. 6559124
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MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

US-09-076-258A-2
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TYPE: amino acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                    Sequence 2, Application US/08484594A

Sequence 2, Application US/08484594A

Batent No. 5714459

GENERAL INFORMATION:
APPLICANT: KISHIMOTO, YABBUO
TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
TITLE OF INVENTION: DERIVED THEREFROM
TITLE OF INVENTION: DERIVED THEREFROM
NUMBER OF SEQUENCES 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.9%; Score 2757.5; DB 1; Length 523; 99.2%; Pred. No. 6.7e-240; tive 2; Mismatches 1; Indels 1;
                                                                                      481 ACPSAHKPLIGTEKCIWGPSYWCONTETAACCNAVEHCKRHVWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCHEVIER: IDN COMPACTED.
OPERATING SYSTEM: DOS
SOFTWARE: PRESEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/484,594A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: 16Tealsen, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/OCKET NUMBER: 29,655
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 523 amino acids TYPE: amino acid sTRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
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Best Local Similarity 99.2
Matches 520; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Sequence 15, Application US/08584671

Sequence 15, Application US/08584671

Batent No. 5910568

GENERAL INFORMATION:
APPLICANT: HAMMESTEDT, ROY H, BARBATO, GUY F,
APPLICANT: CRAMER, PALMER

ITILE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
ITILE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY

NUMBER OF SEQUENCES: 16
CORRESPONDENCES: 18
ADDRESSEE: INTELLECTULAL PROPERTY OFFICE, THE PENNSYLVANIA

ADDRESSEE: STATE UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE INVOLVED IN BINDING OF SPERM
TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
TO ENHANCE OR DECREASE POTENTIAL PERTILITY
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 PGEVCSALNICESLOKHLAELNHOKQLESNKIPELDMTEVVAPFMANIPLLIYPQDGPRS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PGEVC-AINLCESLOKHIAELNHOKQLESNKIPELDMTEVVAPFMANIPLLLYPQDGPRS 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.0%; Score 418.5; DB 1; 98.8%; Pred. No. 3.1e-30; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-027-376-15
; Sequence 15, Application US/09027376
; Patent No. 6004586
; GENERAL INFORMATION:
APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
APPLICANT: CRAMER, PALMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,671
FILING DATE:
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONAHAN, THOMAS J
REGISTATION NUMBER: 29835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UNITED STATES OF AMERICA CAIF: 16802-7000 CANFITER READABLE FORM: MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 KPQPKDNGDVCQDCIQMVTDI 208
255 MMMHMQPKBICALVGFCDBVK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPQPKDNGDVCQDCIQMVTDI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
                              61 MMMHMOPKBICALVGFCDEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: SINGLE TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: NEC 286
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-584-671-15
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APPLICANT: Gill, Parkash S.
APPLICANT: Gill, Parkash S. Gill, N.D., Inc.
TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth FILE REFERENCE: 017986-00041005
FILE REFERENCE: 017986-00041005
CURRENT PAPLICATION NUMBER: US/09/352,548
CURRENT PILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: US 60/092,647
EARLIER FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                 61 LPCDICKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNWSASCKEIVDSYLPVILDI 120
                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKNYISQYSBIAIQMAMHMQPKEICALVGFCDBVKEMPMQTLVPAKVASKNVIPALELVB 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 CKNYISQYSEIAIQMAAHAQPKEICALVGFCDEVKEMPAQTLVPAKVASKNVIPALDLVD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAPDKMCSKLPKSLSEECQEV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 PIKKCHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKWCSKLPKSLSEECQEV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYLD 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 VDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGTLD 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNLBKNSTKQBILAALEKGCSFLPDPYQKQCDQFVABYBPVLIBILVBVMDPSFVCLKIG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 RNLEKNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 479
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                                                                                                                                                            1 MYALFLIASILGAALAGPVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS
                                                                                                                                                                                                                     61 LPCDICKOVVTAAGDMLKDNATERRILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI
                                                                                                                        1 MYALFLLASLLGAALAGPVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS
                                                                                                                                                                                                                                                                                                                           121 IKGEMSRPGEVCSALNICESLOKHLAELNHOKOLESNKIPELDMTEVVAPFMANIPLLLY
                                                                                                                                                                                                                                                                                                                                                                                                                        PODGPRSKPOPKONGDVCQDCIQMVTDIQTAVRTNSTFVQALVBHVKBBCDRLGPGMADI
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                                                                       1;
                 Score 2757.5; DB 2; Length 523;
Pred. No. 6.7e-240;
2; Mismatches 1; Indels 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 ACPSAHKPLLGTEKCIWGPSYWCONTETAAOCNAVEHCKRHVWN 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACPSAHKPLLGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-352-518-2
'Sequence 2, Application US/09352548
'Patent No. 6500431
                       Query Match 98.9%;
Best Local Similarity 99.2%;
Matches 520; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Saposin B
US-09-352-548-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 81; Conserv
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LENGTH: 81
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128 PGEVCSALNLCESLQKHLABLNHQKQLESNKIPELDMTEVVAPFMANIPLLLYPQDGPRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08100247

Patent No. 5571787

GENERAL INFORMATION:
APPLICANT: O'BRIEN, JOHN S.
APPLICANT: TISHHWOTO, YASUO
TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRES ADDRESSE: ANDRESSE: ANDRESSEE: ANDRESSEE: ANDRESSEE: ADDRESSEE: ADDRESSEE: CONTY: NEWPORT BEACH
CITY: NEWPORT BEACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: ELEM PC COMPACIAL
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,247
FILING DATE: 19930730
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ISTACLSOM
REGISTRATION NUMBER: 29,655
REFRENCE/POCKET NUMBER: OBRIEN.002A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                REGISTRATION NUMBER: 29835
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 97.5%;
Matches 79; Conservative
MONAHAN, THOMAS J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 80 amino acide
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                             TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-09-094-192-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
CLONE: SAPOSIN C
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COUNTRY: USA
ZIP: 92660
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1 Sequence 15, Application US/09094192

1 Sequence 15, Application US/09094192

2 Sequence 15, Application US/09094192

3 Patent No. 6103483

4 GENERAL INFORMATION:

APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.

APPLICANT: CRAMER, PALMER

TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PROC

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: INTELLECTULAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY

STREET: 113 TECHNOLOGY CENTER

CITY: UNIVERSITY PARK

STATE: PRONSYLVANIA

COUNTRY: UNITED STATES OF AMERICA

COUNTRY: UNITED STATES OF AMERICA

COUNTRY: NUMITED STATES OF SAMERICA

COUNTRY: NEADABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: NEC 286

OPERATING SYSTEM:

MEDIUM TYPE: STATE: US/09/094,192

SOFFWARE: WORDPERFECT 5.1

CURRENT APPLICATION NUMBER: US/09/094,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 PGEVCSALNICESLQXHLAELNHQXQLESNKIPELDMTEVVAPFMANIPLLLYPQDGPRS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PGEVC-ALNICESLOYHIAELNHQKQLBSNKIPELDMTEVVAPFMANIPLLYPQDGPRS 59
  ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA ADDRESSEE: STATE UNIVERSITY STREET: 113 TECHNOLOGY CENTER CITY: UNIVERSITY PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.8%; Pred. No. 3.1e-30;
Matches 80; Conservative 0; Mismatches 0; Indels
                                                                                      CITY: UNIVERSITY PARK
STATE: PERNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDFERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 KPQPKDNGDVCQDCIQMVTDI 208
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                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MONAHAN, THOMAS J
REGISTRATION NUMBER: 29835
REPERRINCE/DOCKET NUMBER:
TELECHONICION INFORMATION:
TELEPHONE: 814-865-3591
TELEPAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
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1; Length 80; e-29;	0; Indels	311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKSLSEBCOEVVDTYGSSILS 370	DVYCEVCEFLYKEVTKLIDINKTEKEILDAFDKMCSKLPKSLSEECQEVVDTYGSSIL
14.8%; Score 412; DB 1; Length 80; 100.0%; Pred. No. 1.2e-29;	0; Mismatches	DNNKTEKEILDAFDK	DNNKTEKEILDAFDK
14.8%;	ative	LVKEVTKL	LVKEVTKL
Query Match Sest Local Similarity	nes 80; Conservative	311 SDVYCEVCEF	1 SDVYCEVCEF
Query Best	Matches	ò	qq

Search completed: January 13, 2006, 16:36:34 Job time : 55.6556 secs

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; Search time 99.7682 Seconds (without alignments) 2194.512 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                          Run on:
                                                                                                                                                                                                              Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Published Applications AA Main:\*
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
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Database

### SUMMARIES

Description	Sequence 60, Appl Sequence 60, Appl		120						•		Sequence 1871, Ap	Sequence 1873, Ap	Sequence 1878, Ap	Sequence 1879, Ap	_	Sequence 1881, Ap	Sequence 1882, Ap	Sequence 2041, Ap	••	Sequence 1874, Ap	61,	Sequence 61, Appl	Sequence 73, Appl	Sequence 57, Appl	Sequence 1870, Ap	Sequence 1876, Ap	
ID	US-09-870-759-60	US-10-267-502-386	US-10-408-765A-1207	US-10-746-442-23	US-10-428-817A-56	US-10-801-517-1	US-10-473-127-1865	US-10-473-127-1866	US-10-473-127-1868	US-10-473-127-1869	US-10-473-127-1871	US-10-473-127-1873	US-10-473-127-1878	US-10-473-127-1879	US-10-473-127-1880	US-10-473-127-1881	US-10-473-127-1882	US-10-473-127-2041	US-11-036-867-23	US-10-473-127-1874	US-09-870-759-61	US-09-751-708A-61	US-10-060-036-73	US-10-428-817A-57	US-10-473-127-1870	US-10-473-127-1876	
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Sequence 1877, Ap	Sequence 1875, Ap	Sequence 1872, Ap	Sequence 2, Appli	Sequence 38, Appl	Sequence 40, Appl	Sequence 40, Appl	Sequence 176, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 11, Appl	Sequence 903, App	Sequence 1867, Ap	Sequence 340, App	Sequence 8, Appli	Sequence 385, App	Sequence 1959, Ap	Sequence 4529, Ap
US-10-473-127-1877	US-10-473-127-1875	US-10-473-127-1872	US-09-767-007A-2	US-10-618-281-38	US-09-978-418-40	US-10-485-231-40	US-10-205-194-176	US-10-276-162-1	US-11-002-844-1	US-10-452-858C-11	US-09-833-245-903	US-10-473-127-1867	US-10-043-487-340	US-10-332-426-8	US-10-267-502-385	US-11-097-143-1959	US-10-108-260A-4529
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523	526	527	523	522	479	479	554	521	521	227	531	210	209	362	953	953	241
99.4	99.2	99.5	98.9	97.9	87.8	87.8	70.6	43.1	43.1	41.3	40.9	40.3	39.2	29.9	19.8	19.8	19.5
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## ALIGNMENTS

RESULT 1 US-09-870-759-60

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Sequence 60, Application US/09870759

Patent No. US20020177551A1

GRERAL INFORMATION:

APPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

TILLE REFERENCE: 870759

CURRENT APPLICATION NUMBER: US/09/870,759

CURRENT PILING DATE: 2002-01-14

PRIOR PILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 166

SOFTWARE: PATENTIN VERSION 3.1

SEQUENCE: NO COMPOSITION OF SEQ ID NOS: 166

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100.0%; Pred. No. 1.6e-224;
iive 0; Mismatches 0;
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Matches 524; Conservative
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APPLICANT: Fahy, Boin D.
APPLICANT: Fahy, Boin D.
APPLICANT: Ghoso, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Marnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
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100.0%; Pred. No. 1.6e-224;
tive 0; Mismatches 0;
                                                                  APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SEQ ID NO 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1207, Application US/10408765A; Publication No. US20040101874A1; GENERAL INFORMATION:
             Sequence 386, Application US/10267502 Publication No. US20040071700A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 524; Conservative
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US-10-267-502-386
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US-10-408-765A-1207
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100.0%; Score 2789; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                 Sequence 60, Application US/09751708A
Publication No. US20030157113A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR:
TITLE REFERENCE: 751708
CURRENT FILING DATE: 2002-10-15;
PRIOR FILING DATE: 1999-12-28
FRIOR FILING DATE: 1999-12-28
SOFTWARE: Patentin version 3.1
SEQ ID NO 60
LENGTH: 524
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ORGANISM: Homo sapiens
US-09-751-708A-60
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US-09-751-708A-60
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GENERAL INFORMATION:

APPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFRENCE: 38373-189118

CURRENT PILING DATE: 2003-05-05

PRIOR PILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-28

PRIOR PILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01

PRIOR PILING DATE: 2002-10-01

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2003-11-09

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                                                                        Query Match 100.0%; Score 2789; DB 4; Length 524; Best Local Similarity 100.0%; Pred. No. 1.6e-224; Matches 524; Conservative 0; Mismatches 0; Indels 0
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US-10-428-817A-56
Sequence 56, Application US/10428817A
Publication No. US20040214783A1
GENERAL INFORMATION:
  ORGANISM: Homo sapiens
           ; ORGANISM: HOI
US-10-746-442-23
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Sequence 23, Application US/10746442

Sequence 23, Application US/10746442

Publication No. US20040121958A1

GENERAL INFORMATION:

APPLICANT: O'Brien, John S.

TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN FILE REFERENCE: 0726/024001

CURRENT APPLICATION NUMBER: US/10/746,442

CURRENT FILING DATE: 2003-12-24

PRIOR PILING DATE: PILING DATE: 1997-09-11

PRIOR PILING DATE: FILING DATE: 1997-09-11

PRIOR PILING DATE: FILING DATE: 1996-03-05

PRIOR PILING DATE: FILING DATE: 1996-03-05

PRIOR PILING DATE: FILING DATE: 1996-03-05

SOFTWARE: PATENT PILING DATE: FILING DATE: 1996-03-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENT NOS: 25

SOFTWARE: PATENT NOS: 25

TYPE: PRI
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FILE REFERENCE: 660088.465
CURRENT PEPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1207
LENGTH: 524
                                                                                                                                                                                    TYPE: PRT; ORGANISM: Homo sapiens
US-10-408-765A-1207
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LPCDICKOVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI
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Similarity 100.0%; Score 2789; DB 5; Length 524;
Similarity 100.0%; Pred. No. 1.6e-224;
24; Conservative 0; Mismatches 0; Indels 0
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CURRENT APPLICATION NUMBER: US/10/473,127
CURRENT APPLICATION NUMBER: 06/292,64
PRIOR PILING DATE: 2003-09-26
RRIOR PELICATION NUMBER: 60/292,544
PRIOR PILING DATE: 2001-03-28
PRIOR PILING DATE: 2001-05-21
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-09-08
PRIOR PILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR PILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR PILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR PILING DATE: 2001-10-01
PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2001-12-04
PRIOR PILING DATE: 2001-12-04
PRIOR PILING DATE: 2001-12-04
PRIOR PILING DATE: 2001-12-04
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-473-127-1865; Application US/10473127; Sequence 1865, Application US/10473127; Publication No. US20040236091A1; GENERAL INFORMATION:
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US-10-473-127-1865
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Publication No. US20040229799A1

FIGHREAL INFORMATION:
APPLICANT: CALIDIEN'S HOSPITAL MEDICAL
TITLE OF INVENTION: Saposin C-DOPS A Novel Anti-Tumor Agent
TITLE OF INVENTION: Saposin C-DOPS A Novel Anti-Tumor Agent
FILE REFERENCE: CHM09/GN003
CURRENT APPLICATION NUMBER: US/10/801,517

CURRENT FILING DATE: 2004-03-16

PRIOR FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 2

SOFTWARE: PSSEQ for Windows Version 4.0

LENGTH: 524
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                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0
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100.0%; Score 2789; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 524; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
            , ORGANISM: Homo sapiens
US-10-428-817A-56
                                                            Query Match
Best Local Similarity
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US-10-801-517-1
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100.0%; Pred. No. 1.6e-224;
tive 0; Mismatches 0;
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TEANSLATIONAL PROFILING
FILE REFERENCE: 08191-026WO1
CURRENT APPLICATION NUMBER: US/10/473,127
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-10-01
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Publication No. US20040236091A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 524; Conservative
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US-10-473-127-1868
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TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION:
FILE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,127
CURRENT FILING DATE: 2003-09-26
FRIOR PELICATION NUMBER: 60/299,495
FRIOR PILING DATE: 2001-03-28
FRIOR PILING DATE: 2001-05-28
FRIOR APPLICATION NUMBER: 60/395,544
FRIOR APPLICATION NUMBER: 60/395,340
FRIOR APPLICATION NUMBER: 60/30,300
FRIOR PILING DATE: 2001-03-08
FRIOR PILING DATE: 2001-10-01
FRIOR PELICATION NUMBER: 60/336,780
FRIOR PELING DATE: 2001-12-04
FRIOR PELING DATE: 2001-12-04
FRIOR PELING DATE: 2001-12-04
FRIOR PELING DATE: 2001-12-04
FRIOR PELING DATE: 2001-12-04
FRIOR PELING DATE: 2001-12-04
FRIOR PELING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1866, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
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US-10-473-127-1866
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US-10-473-127-1866
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100.0%; Pred. No. 1.6e-224;
ative 0; Mismatches 0;
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PRIOR PILING DATE: 2001-01

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PRIOR FILING DATE: 2001-10-04

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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1871
LENGTH: 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1871, Application US/10473127; Publication No. US20040236091A1; GENERAL INFORMATION:
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US-10-473-127-1871
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Sequence 1869, Application US/10473127

Publication No. US20040236091A1

SEQUENCE INFORMATION:

APPLICANT: Zycos Inc.

TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE SPERENCE: 08191-026W01

CURRENT PILING DATE: 2003-09-26

PRIOR APPLICATION NUMBER: 06/299, 495

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-06-21

PRIOR FILING DATE: 2001-06-21

PRIOR PRILING DATE: 2001-06-08-08

PRIOR FILING DATE: 2001-10-01

PRIOR FILING DATE: 2001-10-01

PRIOR PRILING DATE: 2001-10-01

PRIOR PRING DATE: 2001-10-01

PRIOR PRING DATE: 2001-10-01

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Sequence 1878. Application US/10473127

Publication No. US20040236091A1

GENERAL INPORMATION:

TITLE OF INVENTION: TRANSLATIONAL PROFILING

FILE REPREENCE: 08191-026W01

CURRENT FILING DATE: 2003-09-26

PRIOR APPLICATION NUMBER: 05/279,495

PRIOR APPLICATION NUMBER: 60/279,495

PRIOR APPLICATION NUMBER: 60/279,495

PRIOR APPLICATION NUMBER: 60/295,544

PRIOR APPLICATION NUMBER: 60/326,370

PRIOR PILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-10-01

PRIOR PILING DATE: 2001-10-01

PRIOR PILING DATE: 2001-10-04

PRIOR PILING DATE: 2001-10-04

PRIOR PILING DATE: 2001-10-04

PRIOR PILING DATE: 2001-12-04

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US-10-473-127-1878
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100.0%; Pred. No. 1.6e-224;
vative 0; Mismatches 0;
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Publication No. US20040236091A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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US-10-473-127-1873
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          ACPSAHKPLLGTEKCIMGPSYWCQNTETAAQCNAVEHCKRHVWN
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Job time : 101.768 secs
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                                                                               61 LPCDICKDVVTAAGDMLKONATEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
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; Pred. No. 1.6e-224;
0; Mismatches 0;
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Sequence 1879, Application US/10473127
Publication No. US20040236091A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-06-09
PRIOR FILING DATE: 2001-06-09
PRIOR FILING DATE: 2001-06-09
PRIOR FILING DATE: 2001-06-09
PRIOR PILING DATE: 2001-10-01
PRIOR PILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR PILING DATE: 2001-10-01
PRIOR PILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 2041
SEQ ID NO 1879
SEQ ID NO 1879
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Best Local Similarity 100.
Matches 524; Conservative
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; ORGANISM: Homo sapiens
US-10-473-127-1879
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Sequence Seq

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US-10-81-234-1631

| Sequence 1631, Application US/10821234
| Publication No. US20050255114A1
| Publication No. US20050255114A1
| GENERAL INFORMATION:
| APPLICANT: Labat, Ivan
| APPLICANT: Labat, Ivan
| APPLICANT: Andarmani, Susan
| APPLICANT: Andarmani, Susan
| TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| FILE REFERENCE: 821A
| CURRENT APPLICATION NUMBER: US/10/821,234
| CURRENT FILING DATE: 2004-04-07
| PRIOR PILING DATE: 2003-04-07
| NUMBER OF SEQ ID NOS: 1704
| SOFTWARE: pt SEQ genes Version 1.0
| SEQ ID NO 1631
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100.0%; Pred. No. 4e-211;
ive 0; Mismatches 0; Indels
US-10-821-234-1188
US-10-995-561-776
US-10-995-561-776
US-11-044-899-2
US-11-044-899-2
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US-10-763-712A-70
US-10-878-556A-2
US-10-871-234-1427
US-11-191-374-18
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US-11-191-375-18
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Best Local Similarity 100.
Matches 524; Conservative
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; ORGANISM: Homo sapiens
US-10-821-234-1631
        121
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                                                                                                                                                                                   January 13, 2006, 16:30:30; Search time 10.4106 Seconds (without alignments) 475.862 Million cell updates/sec
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Copyright (c) 1993 - 2006, Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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US-10-995-561-777
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US-10-995-561-771
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 773
LENGTH: 3803
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RNLEKNSTKQEILAALEKGCSPLPDPYQKQCDQPVAEYBPVLIBILVEVMDPSFVCLKIG 480
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Publication No. US20050272054A1
GENERAL INFORMATION:
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US-10-995-561-773
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US-10-995-561-773
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1295 TAQQEMMKPGQAEDSRVLSEQLSQQTALFAEIERNQTKLDQ-----CQKFSQQYSTIVK 1348
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TQPKDGGFCEVCKKLVGYLDRNLEKNSTKQEILAALEKGC-----SFLPDPYQKQ 450
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                                                                                                                                                       g
Sequence 771. Application US/1095561
| Sequence 771. Application US/1095561
| Publication No. US20050272054A1
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al. APPLICANT: CARGILL, Michele et al. TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
| TITLE OF INVENTION: DETECTION AND USES THEREOF
| TITLE OF INVENTION NUMBER: US/10/995,561
| CURRENT APPLICATION NUMBER: US/10/995,561
| NUMBER OF SEQ ID NOS: 85702
| SEQ ID NOS: 85702
| SEQ ID NO 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.1%; Score 113.5; DB 6; 16.3%; Pred. No. 1.4;
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88; Mismatches 191;
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1203 TAQQEMMKPGQAEDSRVLSEQLSQQTALFAEIERNQTKLDQ------CQKFSQQYSTIVK 1256
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 774
LENGTH: 5406
                                                                                                                                                                                                                                                                                                                  71 TAAGDMLKDNATBEE-----ILVYLEKTCDWLPKPNMSASCKEIVDSYLPVIL 118
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                                                                                                                                                                                                                                                         Pred. No. 2.1;
88; Mismatches 191; Indels 133; Gaps
                                                                                                                                                                                                                                        DB 6; Length 5335;
TITLE OF INVENTION: DETECTION AND USES THEREOF FILE REFERENCE: CL001559
                                                                                                                                                                                                                                    4.1%; Score 113.5;
16.3%; Pred. No. 2.1
                                  CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 777
LENGTH: 5335
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Publication No. US20050272054A1
GENERAL INFORMATION:
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1650 CEMMKARHQELL 1661
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                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-995-561-774
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Matches 80; Conserv
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Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GRETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                 D------IIKGEMSRPGEVCSALNLCESLQXHLARL------NHQXQL-- 154
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                                                                                          Gaps
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                                                                                     Indels 133;
    DB 6; Length 5406;
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                                          ; Pred. No. 2.1;
88; Mismatches 191;
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4.1%; Score 113.5; DB 6;
Best Local Similarity 16.3%; Pred. No. 2.1;
Matches 80; Conservative 88; Mismatches 191;
4.1%; Score 113.5; 16.3%; Pred. No. 2.1
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1742 CEMMKARHQELL 1753
                                                                                 80; Conservative
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US-10-995-561-779
                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-995-561-779
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    Query Match
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Sequence 3, Application US/11196400

| Sequence 3, Application US/205028716641
| Publication No. US2005028716641
| GENERAL INFORMATION:
| APPLICANT: DAUBERSIES, PIERRE
| APPLICANT: DAUBERSIES, PIERRE
| APPLICANT: DAUBERSIES, PIERRE
| APPLICANT: DAUBERSIES, PIERRE
| APPLICANTON: MALBER INS/11/196,400
| TITLE OF INVENTION: MALBER: US/11/196,400
| CURRENT FILING DATE: 2005-08-04
| PRIOR FILING DATE: 1996-06-12
| PRIOR PLICATION NUMBER: US/09/742,096
| PRIOR FILING DATE: 1996-06-12
| PRIOR PLIING DATE: 1996-06-12
| PRIOR PLIING DATE: 1996-06-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L----IDNNKTEKEIL-DAPDK-------MCSKLPKELSEECOEVVDTYGSSILS; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 VKEBC---DRLGPGMADICKNYISQYSEIAIQMMMHMQPKEICALVGPCDEVKEMPMQTL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V----PAKVASKAVIPALELVEPIKKHEVPAKSDVYCEVCEFL------VKEVTK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 LPVILDIIKGEMSRPGEVCSALNLCEŞLQKHLAR---LNHQKQLESNKIPELDMTEVVAP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPKOGGFCEVCKKLVGYLDRNLEKNSTKQEILAALEKGC-----SPLPDPYOKQ 450
291 NVIPALELVEPIKKHEVPAK---SDVYCEVCEF--LVKEVIKLIDNNKTE---KBILDAF 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 FMANIPLLLYPQDGPRSKPQPKDNGDVCQDCIQMYTDI-----QTAVRTNSTFVQALVFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTVKSLPC-DICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNMSASCKE-IVDSY
                                                                              DKM--CSKLPKSLSERCQEVVDTYGSSILSILLEFVSPELVCSMLHLCSGTRLPALTVHV
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CEMMKARHQELL 1753
                                                                                                                                                                                                                                                                451 CDQFVAEYEPVL 462
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| Sequence 775, Application US/20050272054A1
| Publication No. US20050272054A1
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al. |
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: DETECTION AND USES THEREOF |
| TITLE OF INVENTION: DETECTION AND USES THEREOF |
| TITLE OF INVENTION: DETECTION AND USES THEREOF |
| TITLE OF INVENTION: DETECTION AND USES THEREOF |
| TITLE OF INVENTION: DETECTION AND USES THEREOF |
| TITLE OF INVENTION: DOTOS: 80702 |
| CURRENT APPLICATION NUMBER: US/10/995,561 |
| CURRENT PRILING DATE: 2004-11-24 |
| NUMBER OF SEQ ID NOS: 86702 |
| SEQ ID NO 775 |
| LENGTH: 5464 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1693 †SVGSSG------GQLLTNLP--GMEQLSGASLEKGALDTTDGYMGVNQAPEKLDKQ 1741
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1469 VLSBELTTKKEQVSEAIKTSOIF---LAKHGHKLSEKEKKQISEQLNALNKAYHDLCDGS 1525
                                                                                                                                                                                                                        401 TOPKOGGFCEVCKKLVGYLDRNLEKNSTKQETLAALEKGC-----SFLPDPYOKQ 450
                                                                                                                                                                                                                                                                                                                                                          343 DKM--CSKLPKSLSEBCOEVVDTYGSSILSILLERVSPBLVCSMLHLCSGTRLPALTVHV 400
                                                                          1409 ALRRLEBEBEKVVEBEKQEHVEKVKELLGWVSTLARNTQGKATSSBTKESTDIEKAILEQQ 1468
                                                                                                                                                                                                245 ISQYSEIAIQM--------MHHMQPKEIÇALVGFCDEVKEMPMQTLVPAKVASK 290
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                                                                                                               --CQDCIQMVTDIQTAVRTNSTFVQALVEH-------VKEECDRLGPGMADICKNY 244
                                       197
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                                         ----BSNKIPB----LDMTEVVAPFMANIPLLLYPQDGPRSKPOPKDNGDV-
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Best Local Similarity 16.34
Matches 80; Conservative
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ORGANISM: Homo sapiens
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Sequence 276. Application US/11124368A
; Sequence 276. Application NO. US20050287559A1
; Bellication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michaele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vaccular Diseases, Methods of Detection and Uses Thereof
; TITLE OF INVENTION: Vaccular Diseases, Methods of Detection and Uses Thereof
; TITLE OF INVENTION: Vaccular Diseases, Methods of Detection and Uses Thereof
; TURENT APPLICATION NUMBER: US/011/124,368A
; CURRENT PILING DATE: 2004-05-07
; PRIOR FILING DATE: 2004-05-07
; PRIOR FILING DATE: 2004-011-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: PRESEQ for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 2036
                                                                                                                                                                                                                    2403 LRKHBELEREVHPIQAQV----ESLEREVGRLCQRSPRAAHGLRHRQQEVAESWWQL-- 2455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2456 ---RSRAQKRREALDALHQAQKLQAMLQBLLVSAQRLRAQMDTSPAPRSPVEARRMLBEH 2512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2513 ----QECKAELDSWTDSISLARSTGQQLLTAGHPFSSDIRQVLAGLEQELSSLEGAWQE 2567
                                                                                                                                                                                                                                                                                                    302 IKKHEV-----PAKSDVYCEVCEFLVKEVTKLIDNN------KTEKEILDAFDKMCS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGGPCEVCK-KLVGYLDRNLEKNSTKQ------BILAALEKGCSFLPDPYQK 449
                                                 CIQMVTDIQTAVRTNSTFVQALVEHVKEECDR---LGPGMADICKNY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                   348 KLPKSLSEBCQEVVDT-YGSSILSILLEE--VSPELVCSMLHLCSGTRLPALTVHVTQPK 404
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                                                                                      2300 FRGNSAGDTVGDACIRSISDLSLQLKNRDP-----EEVKIICQRRSQLNNRWASFHGNL
                                                                                                                                                                         245 ISQYSEIAIQMMMHMQPKEICALVGFCDEVKE--MPMQTLVPAKVASKNVIPALELVEP-
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20.0%; Pred. No. 1.8;
iive 91; Mismatches 191;
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Matches 110; Conserv
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                                                                                                429 KQEILAALEKGCSF-----LPDPYQKQCDQFVAEY---EPVLIEI-----LVEVMDPS 473
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3.9%; Score 108.5; DB 7; Length 3574;
Best Local Similarity 20.3%; Pred. No. 3.2;
Matches 120; Conservative 103; Mismatches 222; Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ABundl, Vinoa
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiachong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
APPLICANT: Zhau, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Dramac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERRNCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT APPLICATION NUMBER: US/21,265
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-17
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-09-15
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NUMBER OF SEQ ID NOS: 944
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      Sequence 454, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Agundi, Vinod
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US-11-000-463-454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 TYKSLPCDI----CKDVVTAAGDMLKDNATEBEILVYLEKTCDWLPKPNMSASCKEIVDSY 113
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                                                                                                                                               425 KNSTKĢEIJAALEKGÇSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVÇLKIGACPS 484
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                                                                                           LEBV-----SPE-LVCSMLHLCSGTRLPALTVHVTOPKDGGFCEVCKKLVGYLDRNLE
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Sequence 281, Application US/11124368A
Publication No. US20050287559A1
GENERAL INFORMATION:
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US-11-124-368A-281
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; Sequence 280, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
    APPLICANT: Michele Cargill
    APPLICANT: James J. Devlin
    APPLICANT: Michele Cargill
    APPLICANT: My Luke
    APPLICANT: My Luke
    TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
    TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses THILE OF INVENTION: Vascular Diseases, Methods of Detection and Uses THILE OF INVENTION: US 60/568,845
    CURRENT FILING DATE: 2004-05-07
    PRIOR FILING DATE: 2004-05-07
    PRIOR FILING DATE: 2004-05-07
    PRIOR FILING DATE: 2004-11-09
    NUMBER OF SEQ ID NOS: 21112
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 280
    LENGTH: 2036
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                                                                                                   326 TKLIDNNKTEKEI-LDAPD-----KMCSKLPKSLSEECQEVVDTYGS--SILSIL 372
                                                                                                                                                          424
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                                              283 VPAKVASKONVIPALELVEPIKKCHEVPAKSD------VYCE--VCEPLVKEV 325
                   HLT------LGKYNEFSVS-LLNEDPKSLDIFIKAVHTTKELYAGMPTI 994
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3.9%; Score 107.5; DB 7;
Best Local Similarity 20.0%; Pred. No. 1.8;
Matches 110; Conservative 91; Mismatches 191;
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US-11-124-368A-280
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QY         373 LEEVSPE-LVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLVGYLDRNLE 424           IIII LELGHKKKGLRSPQILVPTLFNLLSRCLEPLPQEGGNME 1149           QY         425 KNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEVEPVLIEILVBVWDPSFVCLKIGACPS 484           IISOYTKQLILSCLLNICQKL-SPDGGKIPKDILDEEKFNVELIVQCIRLSEMPQ 1199           QY         485 AHKPLLGT 492           IDD         11200 THHHALLLLGT 1210	RESULT 14  US-11-124-588A-277  is Sequence 277, Application US/11124368A  is Sequence 277, Application No. US2050287559A1  is GENERAL INFORMATION:  is APPLICANT: Michaele Cargill  is APPLICANT: May Luke  is TITLE OF INVENTION: Genetic Polymorphisms Associated with  is TITLE OF INVENTION: Qenetic Polymorphisms Associated with  is TITLE OF INVENTION: Usecular Diseases, Methods of Detection and Uses Thereof  is TITLE OF INVENTION: Usecular Diseases, Methods of Detection and Uses THING STILING DATE: 2005-05-09  is PRIOR APPLICATION NUMBER: US 60/568,845  is PRIOR APPLICATION NUMBER: US 60/568,845  is PRIOR APPLICATION NUMBER: US 60/569,845  is PRIOR APPLICATION NUMBER: US 60/569,845  is NUMBER OF SEQ ID NOS: 21112  is SOFTWARE: PastSEQ for Windows Version 4.0  is SEQ ID NO 277  IENGTH: 2144  is TYPE: PRT  is ORGANISM: Homo sapiens	Query Match
Qy         326 TKLIDNNKTEKBI-LDAFDKMCSKLPKSLSEECQEVUDTYGSSILSIL 372           Db         1043 PKGISVNAEQVRIELBPPDKAKPLGTVQQKRQKKSQDLESVQEVGGSYWQRVII 1102           Qy         373 LEEVSPE-LVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKTUGYLDRNLE 424           Db         1103 LELLQHKKGLRSPQILVPTLFNLLSRCLEPLPQEGGNME 1141           Qy         425 KNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIGACFS 484           Db         1142YTKQLILSCLLNICQKL-SPDGGKIPKDILDEEKFNVELIVQCIRLSEMPQ 1191           Qy         485 AHKPLLGT 492	RESULT 13  WS-11-124-368A-278  WS-11-124-368A-278  WS-11-124-368A-278  Sequence 278, Application US/11124368A  PUBLIcation No. US20050287559A1  GENERAL INFORMATION:  APPLICANT: Wichele Cargill  APPLICANT: Wichele Cargill  APPLICANT: Was Devilin  APPLICANT: Was Luke  TITLE OF INVENTION: Vaccular Diseases, Methods of Detection and Uses Thereof  TITLE OF INVENTION: Vaccular Diseases, Methods of Detection and Uses Thereof  FILE REFERENCE: CL001524  CURRENT APPLICATION NUMBER: US/11/124,368A  CURRENT PILING DATE: 2004-05-07  PRIOR APPLICATION NUMBER: US 60/568,845  PRIOR APPLICATION NUMBER: US 60/568,845  PRIOR PILING DATE: 2004-01-09  NUMBER OF SEQ ID NOS: 21112  SEQ ID NO 278  LENGTH: 2044  LENGTH: 2044	US-11-124-368A-178

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US-11-196-400-5

| Sequence 5, Application US/11196400
| Sequence 5, Application No. US20050287166A1
| GENERAL INFORMATION:
| APPLICANT: DAUBERSIES, PIERRE
| APPLICANT: DAUBERSIES, PIERRE
| TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
| TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
| TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
| TILLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
| PRIOR TELING DATE: 1000-10-22
| PRIOR PILING DATE: 1000-10-22
| PRIOR PELING DATE: 1996-06-13
| PRIOR PILING DATE: 1996-06-13
| PRIOR FILING DATE: 1995-06-13
| PRIOR FILING DATE: 1995-06-13
| SEQ ID NO 5
| LENGTH: 630
| TYPE: PRI
| ORGANISM: P. falciparum
| US-11-196-400-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKEILDAFDKWCSKLPKSL--SEECQEVVDTYGSSILSILLEEVSPELVCSMLHLCSGTR 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 VEHYKEEC-----DRLGPGMADICKNYISQYSEIAIQMAMHMOPKEICALVG--FCDEVK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 EMPMQTLVPAKVASKNVIPA-LELVEPIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 PTVKSLPCDICKDVVTAAGDMLKDN---ATERBILVYLEKT----CDWLPKPNMSASCKE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 APFM-----ANIPLILYPQDGPRSKPQPKDNGDVCQDCIQMVTD-IQTAVRTNSTFVQAL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 APTVEESVAPTVEEIVVPSVEESVAESVEES-VAENVEESVAENVEESVAEN-VEESV 338
                                                  -----NME 1249
                             425 KNSTKOBILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIBILVEVMDPSFVCLKIGACPS 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 LPALTVHVTQPKDGGFCEVCKKLVGYLDRNLEKNS--TKQEILAALEK 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || : : : |||: |||
----TVEQAE-----EBSESTITEIPENEBNAVESNEKVAENLEK 528
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3.7%; Score 102; DB 7; Length 630;
Best Local Similarity 18.1%; Pred. No. 1.1;
Matches 74; Conservative 103; Mismatches 155; Indels
   1211 LELLQHKKKLRSPQILVPTLFNLLSRCLEPL------PQEQG---
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                                                                                                                                          1300 THHHALLLIGT 1310
                                                                                                        485 AHKP---LLGT 492
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US-11-196-400-5
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